



SEQUENCE LISTING

#7

<110> Benjanin, Stephane
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

<130> 91.US4.DIV

<140> US 09/992,600

<141> 2001-11-13

<150> US 09/924,340

<151> 2001-08-06

<150> PCT/IB01/01715

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<150> US 60/305,456

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<150> US 60/302,277

<151> 2001-06-29

<150> US 60/298,698

<151> 2001-06-15

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<151> 2001-05-25

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Phe Ser Cys Leu Pro Arg Pro Arg Thr Glu Pro Leu Val Ala Ser Thr
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gac cac acc aaa atg cca tct caa atg gaa cac gcc atg gaa acc atg 1581
Asp His Thr Lys Met Pro Ser Gln Met Glu His Ala Met Glu Thr Met
35 40 45
atg ttt aca ttt cac aaa ttc gct ggg gat aaa ggc tac tta aca aag 1629
Met Phe Thr Phe His Lys Phe Ala Gly Asp Lys Gly Tyr Leu Thr Lys
50 55 60 65
gag gac ctg aga gta ctc atg gaa aag gag ttc cct gga ttt ttg gaa 1677
Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu Glu
70 75 80
aat caa aaa gac cct ctg gct gtg gac aaa ata atg aag gac ctg gac 1725
Asn Gln Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu Asp
85 90 95
cag tgt aga gat ggc aaa gtg ggc ttc cag agc ttc ttt tcc cta att 1773
Gln Cys Arg Asp Gly Lys Val Gly Phe Gln Ser Phe Phe Ser Leu Ile
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Ala Gly Leu Thr Ile Ala Cys Asn Asp Tyr Phe Val Val His Met Lys
115 120 125
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Gln Lys Gly Lys Lys
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Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val	
80 85 90	
ggc act ggg ttc agt tat gtg aat ggt agt ggt gcc tat gcc aag gac	440
Gly Thr Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp	
95 100 105	
ctg gct atg gtg gct tca gac atg atg gtt ctc ctg aag acc ttc ttc	488
Leu Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe	
110 115 120 125	
agt tgc cac aaa gaa ttc cag aca gtt cca ttc tac att ttc tca gag	536
Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser Glu	
130 135 140	
tcc tat gga gga aaa atg gca gct ggc att ggt cta gag ctt tat aag	584
Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu Tyr Lys	
145 150 155	
gcc att cag cga ggg acc atc aag tgc aac ttt gcg ggg gtt gcc ttg	632
Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly Val Ala Leu	
160 165 170	
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Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu Ser Trp Gly Pro	
175 180 185	
tac ctg tac agc atg tct ctt ctc gaa gac aaa ggt ctg gca gag gtg	728
Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys Gly Leu Ala Glu Val	
190 195 200 205	
tct aag gtt gca gag caa gta ctg aat gcc gta aat aag ggg ctc tac	776
Ser Lys Val Ala Glu Gln Val Leu Asn Ala Val Asn Lys Gly Leu Tyr	
210 215 220	
aga gag gcc aca gag ctg tgg ggg aaa gca gaa atg atc att gaa cag	824
Arg Glu Ala Thr Glu Leu Trp Gly Lys Ala Glu Met Ile Ile Glu Gln	
225 230 235	
gta aaa agg gga aac act cag agg cta gcc tgc ttg gct ttt tct ggt	872
Val Lys Arg Gly Asn Thr Gln Arg Leu Ala Cys Leu Ala Phe Ser Gly	
240 245 250	
ggg tac agg gcc cat ggt tgg tgt tgt caa act tgg agt cta cac	917
Gly Tyr Arg Ala His Gly Trp Cys Cys Gln Thr Trp Ser Leu His	
255 260 265	
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10 15 20	
Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn	
25 30 35	
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40 45 50	
Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser	
55 60 65 70	
Asp Leu Lys Pro Arg Lys Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu	

Thr Leu Leu Pro Leu Phe Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu
 25 30 35 40
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 Lys His Tyr Asn Leu Leu Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe
 45 50 55
 tca att gtc act tgatgatata attgcaattt aaactgttaa gctgtgttca 357
 Ser Ile Val Thr
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 taaataaaaa a 438

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 Phe His Glu Lys His His Ser Tyr His Ile Thr Leu Leu Pro Leu Phe
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Met	Thr	Gln	Ser	Pro	Leu	Phe	Leu
5				10			15
tcc	atc	tcc	tgc	agg	tct	agt	cag
Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln
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aac	tat	ttg	gat	tgg	tac	cac	cag
Asn	Tyr	Leu	Asp	Trp	Tyr	His	Gln
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ctg	ata	tac	ttg	ggt	tct	aat	cgg
Leu	Ile	Tyr	Leu	Gly	Ser	Asn	Arg
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agt	ggc	agt	gga	tca	ggc	aca	gat
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
				70			75
gag	gct	gag	gat	gtt	ggg	gtt	tat
Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr
85				90			95
cca	ttc	act	ttc	ggc	cct	ggg	acc
Pro	Phe	Thr	Phe	Gly	Pro	Gly	Thr
				105			110
gct	gca	cca	tct	gtc	ttc	atc	ttc
Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe
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tct	gga	act	gcc	tct	gtt	gtg	tgc
Ser	Gly	Thr	Ala	Ser	Val	Val	Cys
				135			140
gag	gcc	aaa	gta	cag	tgg	aag	gtg
Glu	Ala	Lys	Val	Gln	Trp	Lys	Val
150				155			160
tcc	cag	gag	agt	gtc	aca	gag	cag
Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln
165				170			175
ctc	agc	agc	acc	ctg	acg	ctg	agc
Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser
				185			190
gtc	tac	gcc	tgc	gaa	gtc	acc	cat
Val	Tyr	Ala	Cys	Glu	Val	Thr	His
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aag	agc	ttc	aac	agg	gga	gag	tgt
Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys
				215			220
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 Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser


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65 70 75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
80 85 90
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20 25 30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
35 40 45 50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
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gccctcaggc ctcaggcctt ccttggtttg aagattgggc ttcacctggg acctaccctt 240
tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
-10 -5
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Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
1 5 10 15

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ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
      35      40      45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
      50      55      60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
      65      70      75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
      80      85      90
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Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
      20      25      30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
      35      40      45      50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
      55      60      65
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 tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
 -10 -5
 aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
 1 5 10 15
 atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
 20 25 30
 ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
 35 40 45
 tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
 50 55 60
 ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
 65 70 75
 agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 80 85 90
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 Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
 20 25 30
 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
 35 40 45 50
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
 55 60 65
 Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
 70 75 80
 Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 85 90

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 gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcggggac ccacagcctg 180
 gccctcaggc ytcaggcctt cccaggcttg aagattgggc ttcacctggg acctaccctt 240
 tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
 -10 -5
 aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
 1 5 10 15
 atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
 20 25 30
 ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
 35 40 45
 tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
 50 55 60
 ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
 65 70 75
 agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 80 85 90
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 20 25 30
 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
 35 40 45 50
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
 55 60 65
 Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
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 ctgtggacaa attgaatgta attgatgatg atgtggagga aattaagaaa tcagagcctg 300
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 Met Asp Arg Ala Leu Gln Val Leu Gln
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 Ser Ile Asp Pro Thr Asp Ser Lys Pro Asp Ser Gln Asp Leu Leu Asp
 10 15 20 25
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 Leu Glu Asp Ile Cys Gln Gln Met Gly Pro Met Ile Asp Glu Lys Leu
 30 35 40
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 Glu Glu Ile Asp Arg Lys His Ser Glu Leu Ser Glu Leu Asn Val Lys
 45 50 55
 gtc ctg gaa gct ctg gaa cta tat aac aaa ttg gtg aat gaa gca cca 545
 Val Leu Glu Ala Leu Glu Leu Tyr Asn Lys Leu Val Asn Glu Ala Pro
 60 65 70
 gtg tac tca gtc tat tca aag ctc cac cct cca gca cat tac cca cct 593
 Val Tyr Ser Val Tyr Ser Lys Leu His Pro Pro Ala His Tyr Pro Pro
 75 80 85
 gca tca tct ggg gtt cca atg cag aca tat cca gtt caa tca cat ggt 641
 Ala Ser Ser Gly Val Pro Met Gln Thr Tyr Pro Val Gln Ser His Gly
 90 95 100 105
 gga aac tat atg ggt cag agc att cac caa gta act gtt gcc caa agc 689
 Gly Asn Tyr Met Gly Gln Ser Ile His Gln Val Thr Val Ala Gln Ser
 110 115 120
 tat agc cta gga ccc gat caa att ggt cca ctg aga tct ctg cct cca 737
 Tyr Ser Leu Gly Pro Asp Gln Ile Gly Pro Leu Arg Ser Leu Pro Pro
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 aat gtg aat tcc tca gtg aca gca cag cct gct caa act tca tat tta 785
 Asn Val Asn Ser Ser Val Thr Ala Gln Pro Ala Gln Thr Ser Tyr Leu
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 agc act gga caa gac act gtt tcc aat cct act tat atg aac cag aac 833
 Ser Thr Gly Gln Asp Thr Val Ser Asn Pro Thr Tyr Met Asn Gln Asn
 155 160 165

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Ser Asn Leu Gln Ser Ala Thr Gly Thr Thr Ala Tyr Thr Gln Gln Met	
170 175 180 185	
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Gly Met Ser Val Asp Met Ser Ser Tyr Gln Asn Thr Thr Ser Asn Leu	
190 195 200	
cct caa ctg gca ggc ttt ccg gtg aca gtt cca gct cat cca gtt gca	977
Pro Gln Leu Ala Gly Phe Pro Val Thr Val Pro Ala His Pro Val Ala	
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Gln Gln His Thr Asn Tyr His Gln Gln Pro Leu Leu	
220 225	
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<400> 18

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35 40 45	
Ser Glu Leu Ser Glu Leu Asn Val Lys Val Leu Glu Ala Leu Glu Leu	
50 55 60	
Tyr Asn Lys Leu Val Asn Glu Ala Pro Val Tyr Ser Val Tyr Ser Lys	
65 70 75 80	
Leu His Pro Pro Ala His Tyr Pro Pro Ala Ser Ser Gly Val Pro Met	
85 90 95	
Gln Thr Tyr Pro Val Gln Ser His Gly Gly Asn Tyr Met Gly Gln Ser	
100 105 110	
Ile His Gln Val Thr Val Ala Gln Ser Tyr Ser Leu Gly Pro Asp Gln	
115 120 125	
Ile Gly Pro Leu Arg Ser Leu Pro Pro Asn Val Asn Ser Ser Val Thr	
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145 150 155 160	
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Ser Tyr Gln Asn Thr Thr Ser Asn Leu Pro Gln Leu Ala Gly Phe Pro	
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Met Arg
-15
gcc tgg atc ttc ttt ctc ctt tgc ctg gcc ggg agg gcc ttg gca gcc 165
Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu Ala Ala
-10 -5 1
cct cag caa gaa gcc ctg cct gat gag aca gag gtg gtg gaa gaa act 213
Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu Glu Thr
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gtg gca gag gtg act gag gta tct gtt gga gct aat cct gtc cag gtg 261
Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val Gln Val
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gaa gta gga gaa ttt gat gat ggt gca gag gaa acc gaa gag gag gtg 309
Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu Glu Val
35 40 45 50
gtg gcg gaa aat ccc tgc cag aac cac cac tgc aaa cac ggc aag gtg 357
Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly Lys Val
55 60 65
tgc gag ctg gat gag aac aac acc ccc atg tgc gtg tgc cag gac ccc 405
Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln Asp Pro
70 75 80
acc agc tgc cca gcc ccc att ggc gag ttt gag aag gtg tgc agc aat 453
Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys Ser Asn
85 90 95
gac aac aag acc ttc gac tct tcc tgc cac ttc ttt gcc aca aag tgc 501
Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr Lys Cys
100 105 110
acc ctg gag ggc acc aag aag ggc cac aag ctc cac ctg gac tac atc 549
Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp Tyr Ile
115 120 125 130
ggg cct tgc aaa tac atc ccc cct tgc ctg gac tct gag ctg acc gaa 597
Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu Thr Glu
135 140 145
ttc ccc ctg cgc atg cgg gac tgg ctc aag aac gtc ctg gtc acc ctg 645
Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val Thr Leu
150 155 160
tat gag agg gat gag gac aac aac ctt ctg act gag aag cag aag ctg 693
Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln Lys Leu
165 170 175
cgg gtg aag aag atc cat gag aat gag aag cgc ctg gag gca gga gac 741
Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala Gly Asp
180 185 190
cac ccc gtg gag ctg ctg gcc cgg gac tgc cag gct gtt tca gcc agg 789
His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser Ala Arg
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aag gcc aaa atc aag agt gag atg tagaaagttg taaaatagaa aaagtggagt 843
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<213> Homo sapiens

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gctaaa atg aag act ctg cag tct aca ctt ctc ctg tta ctg ctt gtg      168
      Met Lys Thr Leu Gln Ser Thr Leu Leu Leu Leu Leu Leu Val
              -15                      -10                      -5
cct ctg ata aag cca gca cca cca acc cag cag gac tca cgc att atc      216
Pro Leu Ile Lys Pro Ala Pro Pro Thr Gln Gln Asp Ser Arg Ile Ile
      1                      5                      10

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tat gag gat aaa tac ctg gat gga aaa aat att aag gaa aaa gaa act	312
Tyr Glu Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr	
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gtg ata ata ccc aat gag aaa agt ctt caa tta caa aaa gat gag gca	360
Val Ile Ile Pro Asn Glu Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala	
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ata aca cca tta cct ccc aag aaa gaa aat gat gaa atg ccc acg tgt	408
Ile Thr Pro Leu Pro Pro Lys Lys Glu Asn Asp Glu Met Pro Thr Cys	
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ctg ctg tgt gtt tgt tta agt ggc tct gta tac tgt gaa gaa gtt gac	456
Leu Leu Cys Val Cys Leu Ser Gly Ser Val Tyr Cys Glu Glu Val Asp	
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Ile Asp Ala Val Pro Pro Leu Pro Lys Glu Ser Ala Tyr Leu Tyr Ala	
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cga ttc aac aaa att aaa aag ctg act gcc aaa gat ttt gca gac ata	552
Arg Phe Asn Lys Ile Lys Lys Leu Thr Ala Lys Asp Phe Ala Asp Ile	
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cct aac tta aga aga ctc gat ttt aca gga aat ttg ata gaa gat ata	600
Pro Asn Leu Arg Arg Leu Asp Phe Thr Gly Asn Leu Ile Glu Asp Ile	
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145 150 155	
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Ala Glu Asn Gln Leu Leu Lys Leu Pro Val Leu Pro Pro Lys Leu Thr	
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Leu Phe Asn Ala Lys Tyr Asn Lys Ile Lys Ser Arg Gly Ile Lys Ala	
175 180 185	
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Asn Ala Phe Lys Lys Leu Asn Asn Leu Thr Phe Leu Tyr Leu Asp His	
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aat gcc ctg gaa tcc gtg cct ctt aat tta cca gaa agt cta cgt gta	840
Asn Ala Leu Glu Ser Val Pro Leu Asn Leu Pro Glu Ser Leu Arg Val	
205 210 215 220	
att cat ctt cag ttc aac aac ata gct tca att aca gat gac aca ttc	888
Ile His Leu Gln Phe Asn Asn Ile Ala Ser Ile Thr Asp Asp Thr Phe	
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Cys Lys Ala Asn Asp Thr Ser Tyr Ile Arg Asp Arg Ile Glu Glu Ile	
240 245 250	
cgc ctg gag ggc aat cca atc gtc ctg gga aag cat cca aac agt ttt	984
Arg Leu Glu Gly Asn Pro Ile Val Leu Gly Lys His Pro Asn Ser Phe	
255 260 265	
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Ile Cys Leu Lys Arg Leu Pro Ile Gly Ser Tyr Phe	
270 275 280	
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 aaatgagaat ctcacatcaata aattagttca agcataagat gaaaacagaa tattctgtgg 1930
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 Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr Val Ile
 30 35 40 45
 Ile Pro Asn Glu Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala Ile Thr
 50 55 60
 Pro Leu Pro Pro Lys Lys Glu Asn Asp Glu Met Pro Thr Cys Leu Leu
 65 70 75
 Cys Val Cys Leu Ser Gly Ser Val Tyr Cys Glu Glu Val Asp Ile Asp
 80 85 90
 Ala Val Pro Pro Leu Pro Lys Glu Ser Ala Tyr Leu Tyr Ala Arg Phe
 95 100 105
 Asn Lys Ile Lys Lys Leu Thr Ala Lys Asp Phe Ala Asp Ile Pro Asn
 110 115 120 125
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 130 135 140
 Gly Thr Phe Ser Lys Leu Ser Leu Leu Glu Glu Leu Ser Leu Ala Glu
 145 150 155
 Asn Gln Leu Leu Lys Leu Pro Val Leu Pro Pro Lys Leu Thr Leu Phe
 160 165 170
 Asn Ala Lys Tyr Asn Lys Ile Lys Ser Arg Gly Ile Lys Ala Asn Ala
 175 180 185
 Phe Lys Lys Leu Asn Asn Leu Thr Phe Leu Tyr Leu Asp His Asn Ala
 190 195 200 205
 Leu Glu Ser Val Pro Leu Asn Leu Pro Glu Ser Leu Arg Val Ile His
 210 215 220
 Leu Gln Phe Asn Asn Ile Ala Ser Ile Thr Asp Asp Thr Phe Cys Lys
 225 230 235
 Ala Asn Asp Thr Ser Tyr Ile Arg Asp Arg Ile Glu Glu Ile Arg Leu
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<210> 23
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 1 5 10
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 Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val
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 Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala
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 Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro
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 Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu
 80 85 90
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 Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu
 95 100 105 110
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 Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His
 115 120 125
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 Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp
 130 135 140
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 Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu
 145 150 155
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 Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser
 160 165 170
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 Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val
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 aaa tcc atc aag gca gcc tcc tcc acg gag aag ttc cct gac ggt ttc 675
 Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe
 195 200 205
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 Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp
 210 215 220

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Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val
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255 260 265 270
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Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe
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Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr
320 325 330
gat gag tca acc ctc atg acc ata gcc tat gtc atg gct gcc atc tgc 1107
Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys
335 340 345 350
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Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp Arg Cys
355 360 365
ctc cgc tgc ctg cgc cag cag cat gat gac ttt gct gat gac atc tcc 1203
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370 375 380
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Leu Leu Lys
385
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 <213> Homo sapiens

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 20 25 30
 Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr
 35 40 45
 Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu
 50 55 60

Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Pro	Glu	Pro
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Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser
80					85					90					95
Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu
				100						105				110	
Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu
			115						120				125		
Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr
		130					135					140			
Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met
	145					150					155				
Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr
160					165					170					175
Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser
				180						185					190
Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu
			195						200				205		
Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile
		210					215					220			
Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser
	225					230					235				
Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp
240					245					250					255
Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser
				260					265					270	
Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val
			275					280					285		
Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys
		290					295					300			
His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe	Val
	305					310					315				
Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn	Ile	Pro	Gln	Thr	Asp	Glu
320					325					330					335
Ser	Thr	Leu	Met	Thr	Ile	Ala	Tyr	Val	Met	Ala	Ala	Ile	Cys	Ala	Leu
				340					345					350	
Phe	Met	Leu	Pro	Leu	Cys	Leu	Met	Val	Cys	Gln	Trp	Arg	Cys	Leu	Arg
			355					360					365		
Cys	Leu	Arg	Gln	Gln	His	Asp	Asp	Phe	Ala	Asp	Asp	Ile	Ser	Leu	Leu
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Lys

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 <222> 880..1239

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gccaggagag tcccgcacagg agtgtcaggt ttcaatctca gcaccagcca ctgagagcag 120
ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc 168
      Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
            -20                    -15                    -10
agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca 216
Ser Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
            -5                    1                    5
ctg ctc ggc tcc agc tgg ggt ggc ctg atc cac ctg tac aca gcc aca 264
Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr
            10                    15                    20
gcc agg aac agc tac cac ctg cag atc cac aag aat ggc cat gtg gat 312
Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp
            25                    30                    35
ggc gca ccc cat cag acc atc tac agt gcc ctg atg atc aga tca gag 360
Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu
            40                    45                    50                    55
gat gct ggc ttt gtg gtg att aca ggt gtg atg agc aga aga tac ctc 408
Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu
            60                    65                    70
tgc atg gat ttc aga ggc aac att ttt gga tca cac tat ttc gac ccg 456
Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro
            75                    80                    85
gag aac tgc agg ttc caa cac cag acg ctg gaa aac ggg tac gac gtc 504
Glu Asn Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val
            90                    95                    100
tac cac tct cct cag tat cac ttc ctg gtc agt ctg ggc cgg gcg aag 552
Tyr His Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys
            105                    110                    115
aga gcc ttc ctg cca ggc atg aac cca ccc ccg tac tcc cag ttc ctg 600
Arg Ala Phe Leu Pro Gly Met Asn Pro Pro Tyr Ser Gln Phe Leu
            120                    125                    130                    135
tcc cgg agg aac gag atc ccc cta att cac ttc aac acc ccc ata cca 648
Ser Arg Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro
            140                    145                    150
cgg cgg cac acc cgg agc gcc gag gac gac tgg gag cgg gac ccc ctg 696
Arg Arg His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu
            155                    160                    165
aac gtg ctg aag ccc cgg gcc cgg atg acc ccg gcc ccg gcc tcc tgt 744
Asn Val Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys
            170                    175                    180
tca cag gag ctc ccg agc gcc gag gac aac agc ccg atg gcc agt gac 792
Ser Gln Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp
            185                    190                    195
cca tta ggg gtg gtc agg ggc ggt cga gtg aac acg cac gct ggg gga 840
Pro Leu Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly
            200                    205                    210                    215
acg ggc ccg gaa ggc tgc cgc ccc ttc gcc aag ttc atc tagggctcgt 889
Thr Gly Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
            220                    225
ggaagggcac cctctttaac ccattccctca gcaaacgcag ctcttcccaa ggaccaggtc 949
ccttgacgtt ccgaggatgg gaaaggtgac aggggcatgt atggaatttg ctgcttctct 1009
gggggtccctt ccacaggagg tcctgtgaga accaaccctt gaggcccaag tcatgggggt 1069
tcaccgcctt cctcactcca tatagaacac ctttcccaat aggaaacccc aacaggtaaa 1129
ctagaaattt ccccttcatg aaggtagaga gaaggggtct ctcccaacat atttctcttc 1189
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<213> Homo sapiens

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 Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu
 -5 1 5
 Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg
 10 15 20
 Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala
 25 30 35 40
 Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala
 45 50 55
 Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met
 60 65 70
 Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn
 75 80 85
 Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His
 90 95 100
 Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala
 105 110 115 120
 Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg
 125 130 135
 Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg
 140 145 150
 His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val
 155 160 165
 Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln
 170 175 180
 Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu
 185 190 195 200
 Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
 205 210 215
 Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
 220 225

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<220>
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 <222> 116..961

<220>
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<220>
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 <222> 1164..1179

<220>
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 <222> 116
 <223> Xaa = Asn,Thr

<220>
 <221> UNSURE
 <222> 233
 <223> Xaa = Phe,Ser

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 tgggtctctg actcacttct gacttttaggc gctcgaggac tgtgcccagg agcag atg 118
 Met
 1
 cggtctc agagcc caggtg cgcctg cttgag acccggtgtc aaa cagcaa 166
 Arg Leu Arg Ala Gln Val Arg Leu Leu Glu Thr Arg Val Lys Gln Gln
 5 10 15
 caggtc aagatc aagcag cttttg caggtg aatgaa gtc cagttc ctt 214
 Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe Leu
 20 25 30
 gataaa gga gat gag aat act gtc gtt gat ctt gga agc aag agg cag 262
 Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg Gln
 35 40 45
 tatgca gat tgt tca gag att ttc aat gat ggg tat aag ctc agt gga 310
 Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser Gly
 50 55 60 65
 ttttac aaa atc aaa cct ctc cag agc cca gca gaa ttt tct gtt tat 358
 Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val Tyr
 70 75 80
 tgtgac atgtcc gat gga gga gga tgg act gta att cag aga cga tct 406
 Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg Ser
 85 90 95
 gatggc agtgaa aac ttt aac aga gga tgg aaa gac tat gaa aat ggc 454
 Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn Gly
 100 105 110
 tttgga amt ttt gtc caa aaa cat ggt gaa tat tgg ctg ggc aat aaa 502
 Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn Lys
 115 120 125
 aatctt cac ttc ttg acc act caa gaa gac tac act tta aaa atc gac 550
 Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile Asp
 130 135 140 145
 cttgca gat ttt gaa aaa aat agc cgt tat gca caa tat aag aat ttc 598
 Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn Phe
 150 155 160
 aaagtt gga gat gaa aag aat ttc tac gag ttg aat att ggg gaa tat 646
 Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu Tyr
 165 170 175
 tctgga aca gct gga gat tcc ctt gcg ggg aat ttt cat cct gag gtg 694
 Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu Val
 180 185 190
 cagtgg tgg gct agt cac caa aga atg aaa ttc agc acg tgg gac aga 742
 Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp Arg
 195 200 205
 gatcat gac aac tat gaa ggg aac tgc gca gaa gaa gat cag tct ggc 790
 Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser Gly
 210 215 220 225
 tgg tgg ttt aac agg tgt cac tyt gca aac ctg aat ggt gta tac tac 838
 Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr Tyr
 230 235 240
 agcggc ccc tac acg gct aaa aca gac aat ggg att gtc tgg tac acc 886
 Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr Thr
 245 250 255

tgg cat ggg tgg tgg tat tct ctg aaa tct gtg gtt atg aaa att agg 934
 Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile Arg
 260 265 270
 cca aat gat ttt att cca aat gta att taattgctgc tggtgggctt 981
 Pro Asn Asp Phe Ile Pro Asn Val Ile
 275 280
 tcgtttctgc aattcagctt tgtttaaagt gatttgaaaa atactcattc tgaacatatc 1041
 catgcgcaat catgataact gttgtgagta gtgcttttca ttcttctcac ttgcctttgt 1101
 tacttaatgt gctttcagta cagcagatat gcaatattca ccaaataaat gtagactgtg 1161
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 <213> Homo sapiens

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 <222> 116
 <223> Xaa = Asn,Thr

<220>
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 <222> 233
 <223> Xaa = Phe,Ser

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 20 25 30
 Leu Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg
 35 40 45
 Gln Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser
 50 55 60
 Gly Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val
 65 70 75 80
 Tyr Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg
 85 90 95
 Ser Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn
 100 105 110
 Gly Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn
 115 120 125
 Lys Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile
 130 135 140
 Asp Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn
 145 150 155 160
 Phe Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu
 165 170 175
 Tyr Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu
 180 185 190
 Val Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp
 195 200 205
 Arg Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser
 210 215 220
 Gly Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr
 225 230 235 240
 Tyr Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr
 245 250 255
 Thr Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile
 260 265 270
 Arg Pro Asn Asp Phe Ile Pro Asn Val Ile
 275 280

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 <211> 1118
 <212> DNA
 <213> Homo sapiens

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 <222> 1..344

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 <221> CDS
 <222> 345..1118

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 tggaacaaaa ggaatagtct gcctggaatc cctgcagatc ttggggccgg aggccagtcc 180
 aacccttgga gcaggaagaa acgcaaagtt gtcaagaacc aagtcgagct gcctcagagc 240
 cggcccgag tagctgcaga ctccgcccgc gacgtgtgcg cgcttctctg ggccagagcg 300
 agcctgtttt gtgctcgggt taagagattt gtcccagcta tacc atg ggc cgc act 356
 Met Gly Arg Thr
 cgg gaa gct ggc tgc gtg gcc gct ggt gtg gtt atc ggg gct ggt gcc 404
 Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile Gly Ala Gly Ala
 -15 -10 -5 1
 tgc tac tgt gta tac aga ctg gct tgg gga aga gac gag aac gag aaa 452
 Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp Glu Asn Glu Lys
 5 10 15
 atc tgg gac gaa gac gag gag tct acg gac acc tca gag att ggg gtt 500
 Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser Glu Ile Gly Val
 20 25 30
 gag act gtg aaa gga gct aaa act aac gct ggg gca ggg tct ggg gcc 548
 Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala Gly Ser Gly Ala
 35 40 45
 aaa ctt cag ggt gat tca gag gtc aag cct gag gtg agt ttg gga ctc 596
 Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val Ser Leu Gly Leu
 50 55 60 65
 gag gat tgt ccg ggt gta aaa gag aag gcc cat tca gga tcc cac agc 644
 Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser Gly Ser His Ser
 70 75 80
 gga ggt ggc cta gag gcc aag gcc aag gcc ctt ttc aac acg ctg aag 692
 Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe Asn Thr Leu Lys
 85 90 95
 gaa cag gca agt gca aag gca ggc aaa ggg gct agg gtg ggt acc atc 740
 Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg Val Gly Thr Ile
 100 105 110
 tct ggg aac agg acc ctt gca ccg agt tta ccc tgc cca gga ggc agg 788
 Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys Pro Gly Gly Arg
 115 120 125
 ggt gga ggc tgc cac ccc acc agg agt gga tct agg gcc ggg ggc agg 836
 Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg Ala Gly Gly Arg
 130 135 140 145
 gca agt gga aaa tcc aag gga aag gcc cga agt aag agc acc agg gct 884
 Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys Ser Thr Arg Ala
 150 155 160
 cca gct aca aca tgg cct gtc cgg aga ggc aag ttc aac ttt cct tat 932
 Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe Asn Phe Pro Tyr
 165 170 175
 aaa att gat gat att ctg agt gct ccc gac ctc caa aag gtc ctc aac 980

Lys	Ile	Asp	Asp	Ile	Leu	Ser	Ala	Pro	Asp	Leu	Gln	Lys	Val	Leu	Asn	
		180					185					190				
atc	ctg	gag	cga	aca	aat	gat	cct	ttt	att	caa	gaa	gta	gcc	ttg	gtc	1028
Ile	Leu	Glu	Arg	Thr	Asn	Asp	Pro	Phe	Ile	Gln	Glu	Val	Ala	Leu	Val	
		195				200					205					
act	ctg	ggt	aac	aat	gca	gca	tat	tca	ttt	aac	cag	aat	gcc	ata	cgt	1076
Thr	Leu	Gly	Asn	Asn	Ala	Ala	Tyr	Ser	Phe	Asn	Gln	Asn	Ala	Ile	Arg	
210					215					220					225	
gaa	ttg	ggt	ggt	gtc	cca	att	att	gca	aaa	aaa	aaa	aaa	aaa			1118
Glu	Leu	Gly	Gly	Val	Pro	Ile	Ile	Ala	Lys	Lys	Lys	Lys	Lys			
				230					235							

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 <211> 258
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> 1..20

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Gly	Ala	Gly	Ala	Cys	Tyr	Cys	Val	Tyr	Arg	Leu	Ala	Trp	Gly	Arg	Asp	
				1				5					10			
Glu	Asn	Glu	Lys	Ile	Trp	Asp	Glu	Asp	Glu	Glu	Ser	Thr	Asp	Thr	Ser	
		15				20					25					
Glu	Ile	Gly	Val	Glu	Thr	Val	Lys	Gly	Ala	Lys	Thr	Asn	Ala	Gly	Ala	
	30					35				40						
Gly	Ser	Gly	Ala	Lys	Leu	Gln	Gly	Asp	Ser	Glu	Val	Lys	Pro	Glu	Val	
45					50				55					60		
Ser	Leu	Gly	Leu	Glu	Asp	Cys	Pro	Gly	Val	Lys	Glu	Lys	Ala	His	Ser	
				65				70						75		
Gly	Ser	His	Ser	Gly	Gly	Gly	Leu	Glu	Ala	Lys	Ala	Lys	Ala	Leu	Phe	
		80					85						90			
Asn	Thr	Leu	Lys	Glu	Gln	Ala	Ser	Ala	Lys	Ala	Gly	Lys	Gly	Ala	Arg	
		95				100						105				
Val	Gly	Thr	Ile	Ser	Gly	Asn	Arg	Thr	Leu	Ala	Pro	Ser	Leu	Pro	Cys	
	110					115					120					
Pro	Gly	Gly	Arg	Gly	Gly	Cys	His	Pro	Thr	Arg	Ser	Gly	Ser	Arg		
125					130				135					140		
Ala	Gly	Gly	Arg	Ala	Ser	Gly	Lys	Ser	Lys	Gly	Lys	Ala	Arg	Ser	Lys	
				145					150					155		
Ser	Thr	Arg	Ala	Pro	Ala	Thr	Thr	Trp	Pro	Val	Arg	Arg	Gly	Lys	Phe	
			160					165					170			
Asn	Phe	Pro	Tyr	Lys	Ile	Asp	Asp	Ile	Leu	Ser	Ala	Pro	Asp	Leu	Gln	
	175					180						185				
Lys	Val	Leu	Asn	Ile	Leu	Glu	Arg	Thr	Asn	Asp	Pro	Phe	Ile	Gln	Glu	
	190					195					200					
Val	Ala	Leu	Val	Thr	Leu	Gly	Asn	Asn	Ala	Ala	Tyr	Ser	Phe	Asn	Gln	
205					210					215					220	
Asn	Ala	Ile	Arg	Glu	Leu	Gly	Gly	Val	Pro	Ile	Ile	Ala	Lys	Lys	Lys	
				225					230					235		

Lys Lys

<210> 31
 <211> 1273
 <212> DNA
 <213> Homo sapiens

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<222> 1..13

<220>

<221> CDS

<222> 14..1048

<220>

<221> 3'UTR

<222> 1049..1273

<220>

<221> polyA_signal

<222> 1234..1239

<220>

<221> polyA_site

<222> 1258..1273

<400> 31

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              -25              -20              -15

tgc ggc cag gcg tgg ggt gcg tgc gtg ggc ggc cgc agc tgc gag gag      97
Cys Gly Gln Ala Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu
              -10              -5              1

ctc act gcg gtc cta acc ccg ccg cag ctc ctc gga cgc agg ttt aac     145
Leu Thr Ala Val Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn
              5              10              15

ttc ttt att caa caa aaa tgc gga ttc aga aaa gca ccc agg aag gtt     193
Phe Phe Ile Gln Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val
20              25              30              35

gaa cct cga aga tca gac cca ggg aca agt ggt gaa gca tac aag aga     241
Glu Pro Arg Arg Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg
              40              45              50

agt gct ttg att cct cct gtg gaa gaa aca gtc ttt tat cct tct ccc     289
Ser Ala Leu Ile Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro
              55              60              65

tat cct ata agg agt ctc ata aaa cct tta ttt ttt act gtt ggg ttt     337
Tyr Pro Ile Arg Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe
70              75              80

aca ggc tgt gca ttt gga tca gct gct att tgg caa tat gaa tca ctg     385
Thr Gly Cys Ala Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu
85              90              95

aaa tcc agg gtc cag agt tat ttt gat ggt ata aaa gct gat tgg ttg     433
Lys Ser Arg Val Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu
100              105              110              115

gat agc ata aga cca caa aaa gaa gga gac ttc aga aag gag att aac     481
Asp Ser Ile Arg Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn
              120              125              130

aag tgg tgg aat aac cta agt gat ggc cag cgg act gtg aca ggt att     529
Lys Trp Trp Asn Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile
              135              140              145

ata gct gca aat gtc ctt gta ttc tgt tta tgg aga gta cct tct ctg     577
Ile Ala Ala Asn Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu
150              155              160

cag cgg aca atg atc aga tat ttc aca tcg aat cca gcc tca aag gtc     625
Gln Arg Thr Met Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val
165              170              175

ctt tgt tct cca atg ttg ctg tca aca ttc agt cat ttc tcc tta ttt     673
Leu Cys Ser Pro Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe
180              185              190              195

cac atg gca gca aat atg tat gtt ttg tgg agc ttc tct tcc agc ata     721
His Met Ala Ala Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile
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	200		205		210	
gtg aac att ctg ggt caa gag cag ttc atg gca gtg tac cta tct gca						769
Val Asn Ile Leu Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala						
	215		220		225	
ggg gtt att tcc aat ttt gtc agt tac gtg ggt aaa gtt gcc aca gga						817
Gly Val Ile Ser Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly						
	230		235		240	
aga tat gga cca tca ctt ggt gca gcc ctg aaa gcc att atc gcc atg						865
Arg Tyr Gly Pro Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met						
	245		250		255	
gat aca gca gga atg atc ctg gga tgg aaa ttt ttt gat cat gcg gca						913
Asp Thr Ala Gly Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala						
	260		265		270	275
cat ctt ggg gga gct ctt ttt gga ata tgg tat gtt act tac ggt cat						961
His Leu Gly Gly Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His						
	280		285		290	
gaa ctg att tgg aag aac agg gag ccg cta gtg aaa atc tgg cat gaa						1009
Glu Leu Ile Trp Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu						
	295		300		305	
ata agg act aat ggc ccc aaa aaa gga ggt ggc tct aag taaaactggg						1058
Ile Arg Thr Asn Gly Pro Lys Lys Gly Gly Gly Ser Lys						
	310		315		320	
attggacagt agtggtgcat ctggctccttg ccgcctgaga gcccaggag acatcggcta						1118
gagtgaccat ggctatgctc ccgtctggaa gatgccagca tctggcctcc cacttttttc						1178
agctgtgtcc ccagtcctgt gtcttttttag aatgtgaatg atgataaagt tgtgaaataa						1238
aggtttctat ctagtttgca aaaaaaaaaa aaaaaa						1273

<210> 32

<211> 345

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..26

<400> 32

Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly Cys Gly Gln Ala						
-25	-20		-15			
Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu Leu Thr Ala Val						
-10	-5		1		5	
Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn Phe Phe Ile Gln						
	10		15		20	
Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val Glu Pro Arg Arg						
	25		30		35	
Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg Ser Ala Leu Ile						
	40		45		50	
Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro Tyr Pro Ile Arg						
55	60		65		70	
Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe Thr Gly Cys Ala						
	75		80		85	
Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu Lys Ser Arg Val						
	90		95		100	
Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu Asp Ser Ile Arg						
	105		110		115	
Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn Lys Trp Trp Asn						
	120		125		130	
Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile Ile Ala Ala Asn						
135	140		145		150	
Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu Gln Arg Thr Met						
	155		160		165	
Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val Leu Cys Ser Pro						
	170		175		180	

Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe His Met Ala Ala
 185 190 195
 Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile Val Asn Ile Leu
 200 205 210
 Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala Gly Val Ile Ser
 215 220 225 230
 Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly Arg Tyr Gly Pro
 235 240 245
 Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met Asp Thr Ala Gly
 250 255 260
 Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly
 265 270 275
 Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp
 280 285 290
 Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn
 295 300 305 310
 Gly Pro Lys Lys Gly Gly Gly Ser Lys
 315

<210> 33
 <211> 723
 <212> DNA
 <213> Homo sapiens

<220>
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<220>
 <221> CDS
 <222> 73..672

<220>
 <221> 3'UTR
 <222> 673..723

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 <222> 689..694

<220>
 <221> polyA_site
 <222> 708..723

<400> 33
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 accgacacca tc atg gat tca agc acc gca cac agt ccg gtg ttt ctg gta 111
 Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val
 1 5 10
 ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt tca 159
 Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser
 15 20 25
 gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct aga 207
 Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg
 30 35 40 45
 aaa atg aaa atc tta ggg act atc cag atc ctg ttt gga att atg acc 255
 Lys Met Lys Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr
 50 55 60
 ttt tct ttt gga gtt atc ttc ctt ttc acc ttg tta aaa cca tat cca 303
 Phe Ser Phe Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro
 65 70 75
 agg ttt ccc ttt ata ttt ctt tca gga tat cca ttc tgg ggc tct gtt 351
 Arg Phe Pro Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val

80	85	90	
ttg ttc att aat tct gga gcc ttc cta att gca gtg aaa aga aaa acc			399
Leu Phe Ile Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr			
95	100	105	
aca gaa act ctg ata ata ttg agc cga ata atg aat ttt ctt agt gcc			447
Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala			
110	115	120	125
ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta			495
Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu			
130	135	140	
gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag			543
Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys			
145	150	155	
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc			591
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe			
160	165	170	
agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc			639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys			
175	180	185	
cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata			692
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys			
190	195	200	
aagatgtgtt aaaataaaaa aaaaaaaaaa t			723

<210> 34
 <211> 200
 <212> PRT
 <213> Homo sapiens

<400> 34	
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	20 25 30
Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys	
	35 40 45
Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe	
	50 55 60
Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro	
65	70 75 80
Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile	
	85 90 95
Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr	
	100 105 110
Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala	
	115 120 125
Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn	
	130 135 140
Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr	
145	150 155 160
Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile	
	165 170 175
Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu	
	180 185 190
Asp Cys Asp Cys Glu Gln Cys Cys	
195	200

<210> 35
 <211> 845
 <212> DNA
 <213> Homo sapiens

<220>

<221> 5'UTR
 <222> 1..118

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 <222> 119..655

<220>
 <221> 3'UTR
 <222> 656..845

<220>
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 <222> 809..814

<220>
 <221> polyA_site
 <222> 830..845

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 taaattctgc caaaaggact gaggaacggt gcctggaaaaa gggcaagaat atcacggc 118
 atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc ctg ttt ttc ttc 166
 Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
 1 5 10 15
 aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg ggc ttt ggg atc 214
 Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
 20 25 30
 tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc cat aac ctc ccc 262
 Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
 35 40 45
 tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc tct att atc atg 310
 Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
 50 55 60
 gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag gaa aac aag tgt 358
 Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
 65 70 75 80
 ctg ctt atg tgc ttc ttc atc ctg ctg ctg att atc ctc ctt gct gag 406
 Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
 85 90 95
 gtg acc ttg gcc atc ctg ctc ttt gtg gct aag ggt ctg acc gac agc 454
 Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
 100 105 110
 atc cac cgt tac cac tca gac aat agc acc aag gca gcg tgg gac tcc 502
 Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
 115 120 125
 atc cag tca ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg 550
 Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
 130 135 140
 acc agt ggc cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt 598
 Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
 145 150 155 160
 tgc tat gcg aaa gca aga ctg tgg ttt cat tcc aat ttc ttt att aga 646
 Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
 165 170 175
 ggg cct tat tgatgtgttc taagtctttc cagaaaaaaa ctatccagtg 695
 Gly Pro Tyr
 atttatatcc tgatttcaac cagtcactta gctgataatc acagtaagaa gacttctggt 755
 attatctctc tatcagataa gattttgtta atgtactatt ttactcttca ataaataaaa 815
 cagtttatta tcgcaaaaaa aaaaaaaaaa 845

<210> 36
 <211> 179

<212> PRT

<213> Homo sapiens

<400> 36

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20      25      30
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
35      40      45
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
50      55      60
Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
65      70      75      80
Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
85      90      95
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
100     105     110
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
115     120     125
Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
130     135     140
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
145     150     155     160
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
165     170     175
Gly Pro Tyr
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<210> 37

<211> 517

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..16

<220>

<221> CDS

<222> 17..259

<220>

<221> 3'UTR

<222> 260..517

<400> 37

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      Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu
      1      5      10
gcc ctg tgg gtg acc gtg ggg ctg tct gtc tgt ctc att gca ctg ctg 100
Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu
15      20      25
gtg gcc ctg gct ttc gtg tgc tgg aga aag atc aaa cag agc tgt gag 148
Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu
30      35      40
gag gag aat gca gga gct gag gac cag gat ggg gag gga gaa ggc tcc 196
Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser
45      50      55      60
aag aca gcc ctg cag cct ctg aaa cac tct gac agc aaa gaa gat gat 244
Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp
65      70      75
gga caa gaa ata gcc tgaccatgag gaccaggagg ctgctacccc tcctacagc 299
Gly Gln Glu Ile Ala
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80
tcttaccctc tggctgcaat ggggctgcac tgtgagccct gcccccaaca gatgcatcct 359
gctctgacag gtgggctcct tctccaaagg atgcgataca cagaccactg tgcagcctta 419
tttctccaat ggacatgatt cccaagtcac cctgctgcct tttttcttat agacacaatg 479
aacagaccac ccacaacctt agttctctaa gtcacatcct 517

<210> 38
<211> 81
<212> PRT
<213> Homo sapiens

<400> 38
Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val
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Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala
20 25 30
Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala
35 40 45
Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu
50 55 60
Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile
65 70 75 80
Ala

<210> 39
<211> 1816
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..259

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<222> 260..1048

<220>
<221> 3'UTR
<222> 1049..1816

<220>
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<222> 1782..1787

<220>
<221> polyA_site
<222> 1801..1816

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ggaacctcgg gagcggcagc tccggcgccct ggtagcgaga ggcggggtcc ggagatcccg 120
gcctcaacttc gtcccactgt ggtaggggct gagtcctgcg aatgttaagt gatttgctca 180
aggtgcccac ttgcgaggaa ttggagccca ggccagttct ctgagcctat cattagggct 240
aaaggagtgc gtgatcaga atg gtg tct gga cgg ttc tac ttg tcc tgc ctg 292
Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu
-15 -10
ctg ctg ggg tcc ctg ggc tct atg tgc atc ctc ttc act atc tac tgg 340
Leu Leu Gly Ser Leu Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp
-5 1 5
atg cag tac tgg cgt ggt ggc ttt gcc tgg aat ggc agc atc tac atg 388
Met Gln Tyr Trp Arg Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met
10 15 20

ttc aac tgg cac cca gtg ctt atg gtt gct ggc atg gtg gta ttc tat	436
Phe Asn Trp His Pro Val Leu Met Val Ala Gly Met Val Val Phe Tyr	
25 30 35 40	
gga ggt gcg tca ctg gtg tac cgc ctg ccc cag tgc tgg gtg ggg ccc	484
Gly Gly Ala Ser Leu Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro	
45 50 55	
aaa ctg ccc tgg aaa ctc ctc cat gca gcg ctg cac ctg atg gcc ttc	532
Lys Leu Pro Trp Lys Leu Leu His Ala Ala Leu His Leu Met Ala Phe	
60 65 70	
gtc ctc act gtt gtg ggg ctg gtt gct gtc ttt acg ttt cac aac cat	580
Val Leu Thr Val Val Gly Leu Val Ala Val Phe Thr Phe His Asn His	
75 80 85	
gga agg act gcc aac ctc tac tcc ctt cac agc tgg ctg ggc atc acc	628
Gly Arg Thr Ala Asn Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr	
90 95 100	
act gtc ttc ctc ttc ggc tgc cag tgg ttc ctg ggc ttt gct gtc ttc	676
Thr Val Phe Leu Phe Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe	
105 110 115 120	
ctc ctg ccc tgg gcg tcc atg tgg ctg cgc agc ctc cta aaa cct atc	724
Leu Leu Pro Trp Ala Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile	
125 130 135	
cac gtc ttt ttt gga gcc gcc atc ctc tct ctg tcc atc gca tcc gtc	772
His Val Phe Phe Gly Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val	
140 145 150	
att tgc ggc att aat gag aag ctt ttc ttc agt ttg aaa aac acc acc	820
Ile Ser Gly Ile Asn Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr	
155 160 165	
agg cca tac cac agc ctg ccc agt gag gcg gtc ttt gcc aac agc acc	868
Arg Pro Tyr His Ser Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr	
170 175 180	
ggg atg ctg gtg gtg gcc ttt ggg ctg ctg gtg ctc tac atc ctt ctg	916
Gly Met Leu Val Val Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu	
185 190 195 200	
gct tca tct tgg aag cgc cca gag ccg ggg atc ctg acc gac aga cag	964
Ala Ser Ser Trp Lys Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln	
205 210 215	
ctg ctg cta cag ctg agg cct gga tcc cgg cct ttc cct gtg act tac	1012
Leu Leu Leu Gln Leu Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr	
220 225 230	
gtg tct gtc acc ggc agg cag ccc tac aaa tcc tgg tgacctgctc	1058
Val Ser Val Thr Gly Arg Gln Pro Tyr Lys Ser Trp	
235 240	
tccaagaac agagcctgtc ccagatgtc ccagtagcga tgagtaacag aggtggctgt	1118
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atagggtgga gagcggaag ggtcttgctc ctaagtgttg ctgctgtggc tttttgcct	1478
tctccaaaga cgcactgcca ggtcccaagc ttcagactgc tgtgcttagt aagcaagtga	1538
gaagcctggg gtttgagacc cacctactct ctggcagcat cagcatccta ctctggcaa	1598
catcaggcca acgtccaccc cagcctcaca ttgccagatg ttggcagaag ggctaatt	1658
gaccgtcttg actggctgga gccttcaaag ccaactgggat gtcctccagg cacctgggtc	1718
ccatgaccag ctccccgtct ccataggggt aggcatttca ctgggtttatg aagctcgagt	1778
ttcattaaat atgttaagaa tcaaaaaaaaa aaaaaaaaa	1816

<210> 40

<211> 263

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..20

<400> 40

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          1          5          10
Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met Phe Asn Trp His Pro
          15          20          25
Val Leu Met Val Ala Gly Met Val Val Phe Tyr Gly Gly Ala Ser Leu
          30          35          40
Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro Lys Leu Pro Trp Lys
          45          50          55          60
Leu Leu His Ala Ala Leu His Leu Met Ala Phe Val Leu Thr Val Val
          65          70          75
Gly Leu Val Ala Val Phe Thr Phe His Asn His Gly Arg Thr Ala Asn
          80          85          90
Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr Thr Val Phe Leu Phe
          95          100          105
Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala
          110          115          120
Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile His Val Phe Phe Gly
          125          130          135          140
Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val Ile Ser Gly Ile Asn
          145          150          155
Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr Arg Pro Tyr His Ser
          160          165          170
Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr Gly Met Leu Val Val
          175          180          185
Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu Ala Ser Ser Trp Lys
          190          195          200
Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln Leu Leu Leu Gln Leu
          205          210          215          220
Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr Val Ser Val Thr Gly
          225          230          235
Arg Gln Pro Tyr Lys Ser Trp
          240
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<210> 41

<211> 643

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..90

<220>

<221> CDS

<222> 91..462

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<222> 463..643

<220>

<221> polyA_signal

<222> 607..612

<220>

<221> polyA_site

<222> 628..643

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 Met Pro Ala Cys Arg Leu Gly Pro
 -25
 cta gcc gcc gcc ctc ctc ctc agc ctg ctg ctg ttc ggc ttc acc cta 162
 Leu Ala Ala Ala Leu Leu Leu Ser Leu Leu Leu Phe Gly Phe Thr Leu
 -20 -15 -10
 gtc tca ggc aca gga gca gag aag act ggc gtg tgc ccc gag ctc cag 210
 Val Ser Gly Thr Gly Ala Glu Lys Thr Gly Val Cys Pro Glu Leu Gln
 -5 1 5 10
 gct gac cag aac tgc acg caa gag tgc gtc tgc gac agc gaa tgc gcc 258
 Ala Asp Gln Asn Cys Thr Gln Glu Cys Val Ser Asp Ser Glu Cys Ala
 15 20 25
 gac aac ctc aag tgc tgc agc gcg ggc tgt gcc acc ttc tgc tct ctg 306
 Asp Asn Leu Lys Cys Cys Ser Ala Gly Cys Ala Thr Phe Cys Ser Leu
 30 35 40
 ccc aat gat aag gag ggt tcc tgc ccc cag gtg aac att aac ttt ccc 354
 Pro Asn Asp Lys Glu Gly Ser Cys Pro Gln Val Asn Ile Asn Phe Pro
 45 50 55
 cag ctc ggc ctc tgt cgg gac cag tgc cag gtg gac agc cag tgt cct 402
 Gln Leu Gly Leu Cys Arg Asp Gln Cys Gln Val Asp Ser Gln Cys Pro
 60 65 70 75
 ggc cag atg aaa tgc tgc cgc aat ggc tgt ggg aag gtg tcc tgt gtc 450
 Gly Gln Met Lys Cys Cys Arg Asn Gly Cys Gly Lys Val Ser Cys Val
 80 85 90
 act ccc aat ttc tgagctccag ccaccaccag gctgagcagt gaggagagaa 502
 Thr Pro Asn Phe
 95
 agttttctgcc tggccctgca tctgggttcca gcccacctgc cctcccccttt ttccgggactc 562
 tgtattccct cttaggctga ccacagcttc tccctttccc aaccaataaa gtaaccactt 622
 tcagcaaaaa aaaaaaaaaa a 643

<210> 42
 <211> 124
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..30

<400> 42
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 -30 -25 -20 -15
 Leu Leu Leu Phe Gly Phe Thr Leu Val Ser Gly Thr Gly Ala Glu Lys
 -10 -5 1
 Thr Gly Val Cys Pro Glu Leu Gln Ala Asp Gln Asn Cys Thr Gln Glu
 5 10 15
 Cys Val Ser Asp Ser Glu Cys Ala Asp Asn Leu Lys Cys Cys Ser Ala
 20 25 30
 Gly Cys Ala Thr Phe Cys Ser Leu Pro Asn Asp Lys Glu Gly Ser Cys
 35 40 45 50
 Pro Gln Val Asn Ile Asn Phe Pro Gln Leu Gly Leu Cys Arg Asp Gln
 55 60 65
 Cys Gln Val Asp Ser Gln Cys Pro Gly Gln Met Lys Cys Cys Arg Asn
 70 75 80
 Gly Cys Gly Lys Val Ser Cys Val Thr Pro Asn Phe
 85 90

<210> 43
 <211> 501
 <212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..227

<220>

<221> CDS

<222> 228..501

<400> 43

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agttgtctca tcattggtgg cttaaaatga tgtttttgaa caagaagaca ccccatggga 120
ctgatctcaa atgcagctgt gactaaaacc tctaggtgct gtgctgtcct gaggcctggg 180
ccatggtgcc caaggaaagc ccctgaagct caccaggagg aagaagc atg cag ggc 236
                                     Met Gln Gly
                                     -30
act cct gga ggc ggg acg cgc cct ggg cca tcc ccc gtg gac agg cgg 284
Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val Asp Arg Arg
                                     -25               -20               -15
aca ctc ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg 332
Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met
                                     -10               -5               1
aat ttc aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag 380
Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Glu Lys
      5               10               15
cag ctt tca ctt ctc ggg gat ctg gag ggc ctg aaa ccc cag aag gtg 428
Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val
20               25               30               35
gac ttc tgg cgt ggc cca gcc agg ccc agc ctc cct gtg gat atg aga 476
Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg
      40               45               50
gtt cct ttc tcc gaa ctg aaa gac a 501
Val Pro Phe Ser Glu Leu Lys Asp
      55
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<210> 44

<211> 91

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..33

<400> 44

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                                     -30               -25               -20
Asp Arg Arg Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu
                                     -15               -10               -5
Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys
      1               5               10               15
Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro
      20               25               30
Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val
      35               40               45
Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp
      50               55
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<210> 45

<211> 960

<212> DNA

<213> Homo sapiens

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 <222> 1..97

<220>
 <221> CDS
 <222> 98..934

<220>
 <221> 3'UTR
 <222> 935..960

<400> 45
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 cggcccgttt caccocgagg aggaaggaca ctgggtc atg acg cca tca gaa ggc 115
 Met Thr Pro Ser Glu Gly
 1 5
 gcc aga gca ggg acc gga cgc gag ttg gag atg ttg gac tcg ctg ttg 163
 Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu Met Leu Asp Ser Leu Leu
 10 15 20
 gcc ttg ggc ggc ctg gtg ctg ctt cgg gat tcc gtg gag tgg gag ggg 211
 Ala Leu Gly Gly Leu Val Leu Leu Arg Asp Ser Val Glu Trp Glu Gly
 25 30 35
 cgc agt ctc ttg aag gcg ctt gtc aag aaa tct gca ctg tgt ggg gag 259
 Arg Ser Leu Leu Lys Ala Leu Val Lys Lys Ser Ala Leu Cys Gly Glu
 40 45 50
 caa gtg cat atc ctg ggc tgt gaa gtg agc gag gaa gag ttt cgt gaa 307
 Gln Val His Ile Leu Gly Cys Glu Val Ser Glu Glu Glu Phe Arg Glu
 55 60 65 70
 ggt ttt gac tct gat atc aac aat cgg ctg gtt tac cat gac ttc ttc 355
 Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu Val Tyr His Asp Phe Phe
 75 80 85
 aga gac cct ctc aac tgg tca aaa act gag gag gcc ttt cct ggg ggg 403
 Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu Glu Ala Phe Pro Gly Gly
 90 95 100
 ccg ctg gga gcc ttg aga gcc atg tgc aag agg aca gat cct gtt cct 451
 Pro Leu Gly Ala Leu Arg Ala Met Cys Lys Arg Thr Asp Pro Val Pro
 105 110 115
 gtc acc att gct ctc gat tca ctc agc tgg ctg cta ctt cgc ctt ccc 499
 Val Thr Ile Ala Leu Asp Ser Leu Ser Trp Leu Leu Leu Arg Leu Pro
 120 125 130
 tgc acc aca ctc tgc cag gtc ctg cat gct gtg agc cat cag gac tct 547
 Cys Thr Thr Leu Cys Gln Val Leu His Ala Val Ser His Gln Asp Ser
 135 140 145 150
 tgt cct ggt gac agc tcc tca gtg ggg aaa gtg agt gtg ctg ggc ttg 595
 Cys Pro Gly Asp Ser Ser Ser Val Gly Lys Val Ser Val Leu Gly Leu
 155 160 165
 cta cat gaa gag ctt cat gga cca ggc cct gtg gga gct ctc agc agc 643
 Leu His Glu Glu Leu His Gly Pro Gly Pro Val Gly Ala Leu Ser Ser
 170 175 180
 ctt gct cag act gag gtg acc ctg ggc ggt acc atg ggc cag gcc tcg 691
 Leu Ala Gln Thr Glu Val Thr Leu Gly Gly Thr Met Gly Gln Ala Ser
 185 190 195
 gcc cac atc ctg tgt cgg agg ccc cga cag cgc cca act gac cag act 739
 Ala His Ile Leu Cys Arg Arg Pro Arg Gln Arg Pro Thr Asp Gln Thr
 200 205 210
 cag tgg ttc tcc atc ctt ccg gac ttc agc ctg gat ctc caa gag ggg 787
 Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser Leu Asp Leu Gln Glu Gly
 215 220 225 230
 ccc tct gta gag tcc cag ccc tac tcc gat cct cat ata ccc ccg gta 835
 Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp Pro His Ile Pro Pro Val
 235 240 245

tct aag aat gcc aag gcc aga aca agg aaa tgt agt tta gta tct ggt	883
Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys Cys Ser Leu Val Ser Gly	
250 255 260	
cac ggg aga gaa aat aaa agc tgc aga ggt tgg ggg tgg ggt cag gga	931
His Gly Arg Glu Asn Lys Ser Cys Arg Gly Trp Gly Trp Gly Gln Gly	
265 270 275	
ttc tagggatggg gcagagtggc agcatc	960
Phe	

<210> 46
 <211> 279
 <212> PRT
 <213> Homo sapiens

<400> 46	
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20 25 30	
Ser Val Glu Trp Glu Gly Arg Ser Leu Leu Lys Ala Leu Val Lys Lys	
35 40 45	
Ser Ala Leu Cys Gly Glu Gln Val His Ile Leu Gly Cys Glu Val Ser	
50 55 60	
Glu Glu Glu Phe Arg Glu Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu	
65 70 75 80	
Val Tyr His Asp Phe Phe Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu	
85 90 95	
Glu Ala Phe Pro Gly Gly Pro Leu Gly Ala Leu Arg Ala Met Cys Lys	
100 105 110	
Arg Thr Asp Pro Val Pro Val Thr Ile Ala Leu Asp Ser Leu Ser Trp	
115 120 125	
Leu Leu Leu Arg Leu Pro Cys Thr Thr Leu Cys Gln Val Leu His Ala	
130 135 140	
Val Ser His Gln Asp Ser Cys Pro Gly Asp Ser Ser Ser Val Gly Lys	
145 150 155 160	
Val Ser Val Leu Gly Leu Leu His Glu Glu Leu His Gly Pro Gly Pro	
165 170 175	
Val Gly Ala Leu Ser Ser Leu Ala Gln Thr Glu Val Thr Leu Gly Gly	
180 185 190	
Thr Met Gly Gln Ala Ser Ala His Ile Leu Cys Arg Arg Pro Arg Gln	
195 200 205	
Arg Pro Thr Asp Gln Thr Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser	
210 215 220	
Leu Asp Leu Gln Glu Gly Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp	
225 230 235 240	
Pro His Ile Pro Pro Val Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys	
245 250 255	
Cys Ser Leu Val Ser Gly His Gly Arg Glu Asn Lys Ser Cys Arg Gly	
260 265 270	
Trp Gly Trp Gly Gln Gly Phe	
275	

<210> 47
 <211> 1294
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..266

<220>
 <221> CDS

<222> 267..1139

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<221> 3'UTR

<222> 1140..1294

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<221> polyA_signal

<222> 1246..1251

<220>

<221> polyA_site

<222> 1279..1294

<400> 47

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aaattcttac ctgcgtcttt cactgctagt aagatcagat tgcgtttctt tcagttactc 120
ttcaatcgcc agtttcttga tctgcttcta aaagaagaag tagagaagat aaatcctgtc 180
ttcaatacct ggaaggaaaa acaaaataac ctcaactccg ttttgaaaaa aacattccaa 240
gaactttcat cagagatttt acttag atg att tac aca atg aag aaa gta cat 293
                                Met Ile Tyr Thr Met Lys Lys Val His
                                -25                                -20
gca ctt tgg gct tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct 341
Ala Leu Trp Ala Ser Val Cys Leu Leu Leu Asn Leu Ala Pro Ala Pro
                                -15                                -10                                -5
ctt aat gct gat tct gag gaa gat gaa gaa cac aca att atc aca gat 389
Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp
                                1                                5                                10
acg gag ttg cca cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag 437
Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys
15                                20                                25                                30
gcg gat gat ggc cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat 485
Ala Asp Asp Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn
                                35                                40                                45
att ttc act cga cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga 533
Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly
                                50                                55                                60
aat cag aat cga ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca 581
Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr
                                65                                70                                75
aga gaa aag cca gat ttc tgc ttt ttg gaa gaa gat cct gga ata tgt 629
Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys
80                                85                                90
cga ggt tat att acc agg tat ttt tat aac aat cag aca aaa cag tgt 677
Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys
95                                100                                105                                110
gaa cgt ttc aag tat ggt gga tgc ctg ggc aat atg aac aat ttt gag 725
Glu Arg Phe Lys Tyr Gly Gly Cys Leu Asn Met Asn Asn Phe Glu
                                115                                120                                125
aca ctg gaa gaa tgc aag aac att tgt gaa gat ggt ccg aat ggt ttc 773
Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe
                                130                                135                                140
cag gtg gat aat tat gga acc cag ctc aat gct gtg aat aac tcc ctg 821
Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn Ala Val Asn Asn Ser Leu
145                                150                                155
act ccg caa tca acc aag gtt ccc agc ctt ttt gaa ttt cac ggt ccc 869
Thr Pro Gln Ser Thr Lys Val Pro Ser Leu Phe Glu Phe His Gly Pro
160                                165                                170
tca tgg tgt ctc act cca gca gac aga gga ttg tgt cgt gcc aat gag 917
Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu
175                                180                                185                                190
aac aga ttc tac tac aat tca gtc att ggg aaa tgc cgc cca ttt aag 965
Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe Lys
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          195          200          205
tac agt gga tgt ggg gga aat gaa aac aat ttt act tcc aaa caa gaa 1013
Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu
          210          215          220
tgt ctg agg gca tgt aaa aaa ggt ttc atc caa aga ata tca aaa gga 1061
Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly
          225          230          235
ggc cta att aaa acc aaa aga aaa aga aag aag cag aga gtg aaa ata 1109
Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys Lys Gln Arg Val Lys Ile
          240          245          250
gca tat gaa gaa att ttt gtt aaa aat atg tgaatttggt atagcaatgt 1159
Ala Tyr Glu Glu Ile Phe Val Lys Asn Met
          255          260
aacattaatt ctactaaata ttttatatga aatggtttcac tatgattttc tattttttctt 1219
ctaaaatgct tttaattaat atgttcatta aatttttctat gottatttgta cttgtttacca 1279
aaaaaaaaaa aaaaaa 1294

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<210> 48
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..28

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<400> 48
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Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu
          -10          -5          1
Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
5          10          15          20
Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys
          25          30          35
Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
          40          45          50
Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
          55          60          65
Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys
70          75          80
Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
85          90          95          100
Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
          105          110          115
Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn
          120          125          130
Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr
          135          140          145
Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val
          150          155          160
Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala
165          170          175          180
Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser
          185          190          195
Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn
          200          205          210
Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys
          215          220          225
Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg
          230          235          240
Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val
245          250          255          260

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Lys Asn Met

<210> 49
 <211> 1194
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..47

<220>
 <221> CDS
 <222> 48..1100

<220>
 <221> 3'UTR
 <222> 1101..1194

<220>
 <221> polyA_signal
 <222> 1159..1164

<220>
 <221> polyA_site
 <222> 1179..1194

<400> 49
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 Met Pro Ser
 tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104
 Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
 -20 -15 -10 -5
 cct gtc tcc ctg ggg acc aag gct gac act cac gat gaa atc ctg gag 152
 Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu
 1 5 10
 ggc ctg aat ttc aac ctc acg gag att ccg gag gct cag atc cat gaa 200
 Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu
 15 20 25
 ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac agc cag ctc 248
 Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu
 30 35 40
 cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc ctg aag cta 296
 Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu
 45 50 55 60
 gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac tca gaa gcc 344
 Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala
 65 70 75
 ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa cag atc aac 392
 Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn
 80 85 90
 gat tac gtg gag aag ggt act caa ggg aaa att gtg gat ttg gtc aag 440
 Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys
 95 100 105
 gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac atc ttc ttt 488
 Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe
 110 115 120
 aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc gag gaa gag 536
 Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu
 125 130 135 140
 gac ttc cac gtg gac cag gtg acc acc gtg aag gtg cct atg atg aag 584
 Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys
 145 150 155

cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg tcc agc tgg	632
Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp	
160 165 170	
gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc ttc ttc ctg	680
Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu	
175 180 185	
cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc acc cac gat	728
Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp	
190 195 200	
atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct gcc agc tta	776
Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu	
205 210 215 220	
cat tta ccc aaa ctg tcc att act gga acc tat gat ctg aag agc gtc	824
His Leu Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu Lys Ser Val	
225 230 235	
ctg ggt caa ctg ggc atc act aag gtc ttc agc aat ggg gct gac ctc	872
Leu Gly Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly Ala Asp Leu	
240 245 250	
tcc ggg gtc aca gag gag gca ccc ctg aag ctc tcc aag gcc gtg cat	920
Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys Ala Val His	
255 260 265	
aag gct gtg ctg acc atc gac gag aaa ggg act gaa gct gct ggg gcc	968
Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala	
270 275 280	
atg ttt tta gag gcc ata ccc atg tct atc ccc ccc gag gtc aag ttc	1016
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe	
285 290 295 300	
aac aaa ccc ttt gtc ttc tta atg att gac caa aat acc aag tct ccc	1064
Asn Lys Pro Phe Val Phe Leu Met Ile Asp Gln Asn Thr Lys Ser Pro	
305 310 315	
ctc ttc atg gga aaa gtg gtg aat ccc acc caa aaa taactgcctc	1110
Leu Phe Met Gly Lys Val Val Asn Pro Thr Gln Lys	
320 325	
tcgtctctca acccctcccc tccatccctg gccccctccc tggatgacat taaagaagg	1170
ttgagctgaa aaaaaaaaaa aaaa	1194

<210> 50
 <211> 351
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

<400> 50
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 Cys Leu Val Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu
 -5 1 5
 Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln
 10 15 20
 Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp
 25 30 35 40
 Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly
 45 50 55
 Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His
 60 65 70
 Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys
 75 80 85
 Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp
 90 95 100
 Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr

105					110					115				120
Ile	Phe	Phe	Lys	Gly	Lys	Trp	Glu	Arg	Pro	Phe	Glu	Val	Lys	Asp
				125					130					135
Glu	Glu	Glu	Asp	Phe	His	Val	Asp	Gln	Val	Thr	Thr	Val	Lys	Val
			140					145					150	
Met	Met	Lys	Arg	Leu	Gly	Met	Phe	Asn	Ile	Gln	His	Cys	Lys	Leu
		155					160					165		
Ser	Ser	Trp	Val	Leu	Leu	Met	Lys	Tyr	Leu	Gly	Asn	Ala	Thr	Ala
		170				175					180			
Phe	Phe	Leu	Pro	Asp	Glu	Gly	Lys	Leu	Gln	His	Leu	Glu	Asn	Glu
185				190					195					200
Thr	His	Asp	Ile	Ile	Thr	Lys	Phe	Leu	Glu	Asn	Glu	Asp	Arg	Arg
			205						210				215	
Ala	Ser	Leu	His	Leu	Pro	Lys	Leu	Ser	Ile	Thr	Gly	Thr	Tyr	Asp
		220						225					230	
Lys	Ser	Val	Leu	Gly	Gln	Leu	Gly	Ile	Thr	Lys	Val	Phe	Ser	Asn
		235					240					245		
Ala	Asp	Leu	Ser	Gly	Val	Thr	Glu	Glu	Ala	Pro	Leu	Lys	Leu	Ser
	250					255				260				
Ala	Val	His	Lys	Ala	Val	Leu	Thr	Ile	Asp	Glu	Lys	Gly	Thr	Glu
265				270					275					280
Ala	Gly	Ala	Met	Phe	Leu	Glu	Ala	Ile	Pro	Met	Ser	Ile	Pro	Pro
			285					290					295	
Val	Lys	Phe	Asn	Lys	Pro	Phe	Val	Phe	Leu	Met	Ile	Asp	Gln	Asn
		300					305					310		
Lys	Ser	Pro	Leu	Phe	Met	Gly	Lys	Val	Val	Asn	Pro	Thr	Gln	Lys
		315				320						325		

<210> 51
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 <212> DNA
 <213> Homo sapiens

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<220>
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 <222> 290..1162

<220>
 <221> 3'UTR
 <222> 1163..1317

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 <222> 1269..1274

<220>
 <221> polyA_site
 <222> 1302..1317

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 cgacttttagg ctggataata gtcaaattct tacctcgctc tttcactgct agtaagatca 120
 gattgcgttt ctttcagtta ctcttcaatc gccagtttct tgatctgctt ctaaaagaag 180
 aagtagagaa gataaatcct gtcttcaata cctggaagga aaaacaaaat aacctcaact 240
 ccggttttgaa aaaaacattc caagaacttt catcagagat tttacttag atg att tac 298
 Met Ile Tyr
 -25
 aca atg aag aaa gta cat gca ctt tgg gct tct gta tgc ctg ctg ctt 346
 Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys Leu Leu Leu

				-20					-15					-10			
aat	ctt	gcc	cct	gcc	cct	ctt	aat	gct	gat	tct	gag	gaa	gat	gaa	gaa		394
Asn	Leu	Ala	Pro	Ala	Pro	Leu	Asn	Ala	Asp	Ser	Glu	Glu	Asp	Glu	Glu		
			-5					1				5					
cac	aca	att	atc	aca	gat	acg	gag	ttg	cca	cca	ctg	aaa	ctt	atg	cat		442
His	Thr	Ile	Ile	Thr	Asp	Thr	Glu	Leu	Pro	Pro	Leu	Lys	Leu	Met	His		
	10					15					20						
tca	ttt	tgt	gca	ttc	aag	tcg	gat	gat	ggc	cca	tgt	aaa	gca	atc	atg		490
Ser	Phe	Cys	Ala	Phe	Lys	Ser	Asp	Asp	Gly	Pro	Cys	Lys	Ala	Ile	Met		
	25				30				35				40				
aaa	aga	ttt	ttc	ttc	aat	att	ttc	act	cga	cag	tgc	gaa	gaa	ttt	ata		538
Lys	Arg	Phe	Phe	Phe	Asn	Ile	Phe	Thr	Arg	Gln	Cys	Glu	Glu	Phe	Ile		
			45					50					55				
tat	ggg	gga	tgt	gaa	gga	aat	cag	aat	cga	ttt	gaa	agt	ctg	gaa	gag		586
Tyr	Gly	Gly	Cys	Glu	Gly	Asn	Gln	Asn	Arg	Phe	Glu	Ser	Leu	Glu	Glu		
			60					65					70				
tgc	aaa	aaa	atg	tgt	aca	aga	gaa	aag	cca	gat	ttc	tgc	ttt	ttg	gaa		634
Cys	Lys	Lys	Met	Cys	Thr	Arg	Glu	Lys	Pro	Asp	Phe	Cys	Phe	Leu	Glu		
	75						80				85						
gaa	gat	cct	gga	ata	tgt	cga	ggg	tat	att	acc	agg	tat	ttt	tat	aac		682
Glu	Asp	Pro	Gly	Ile	Cys	Arg	Gly	Tyr	Ile	Thr	Arg	Tyr	Phe	Tyr	Asn		
	90					95					100						
aat	cag	aca	aaa	cag	tgt	gaa	cgt	ttc	aag	tat	ggg	gga	tgc	ctg	ggc		730
Asn	Gln	Thr	Lys	Gln	Cys	Glu	Arg	Phe	Lys	Tyr	Gly	Gly	Cys	Leu	Gly		
	105				110				115					120			
aat	atg	aac	aat	ttt	gag	aca	ctg	gaa	gaa	tgc	aag	aac	att	tgt	gaa		778
Asn	Met	Asn	Asn	Phe	Glu	Thr	Leu	Glu	Glu	Cys	Lys	Asn	Ile	Cys	Glu		
				125				130					135				
gat	ggg	ccg	aat	ggg	ttc	cag	gtg	gat	aat	tat	gga	acc	cag	ctc	aat		826
Asp	Gly	Pro	Asn	Gly	Phe	Gln	Val	Asp	Asn	Tyr	Gly	Thr	Gln	Leu	Asn		
			140					145					150				
gct	gtg	aat	aac	tcc	ctg	act	ccg	caa	tca	acc	aag	gtt	ccc	agc	ctt		874
Ala	Val	Asn	Asn	Ser	Leu	Thr	Pro	Gln	Ser	Thr	Lys	Val	Pro	Ser	Leu		
		155					160					165					
ttt	gaa	ttt	cac	ggg	ccc	tca	tgg	tgt	ctc	act	cca	gca	gac	aga	gga		922
Phe	Glu	Phe	His	Gly	Pro	Ser	Trp	Cys	Leu	Thr	Pro	Ala	Asp	Arg	Gly		
	170				175						180						
ttg	tgt	cgt	gcc	aat	gag	aac	aga	ttc	tac	tac	aat	tca	gtc	att	ggg		970
Leu	Cys	Arg	Ala	Asn	Glu	Asn	Arg	Phe	Tyr	Tyr	Asn	Ser	Val	Ile	Gly		
	185				190				195					200			
aaa	tgc	cgc	cca	ttt	aag	tac	agt	gga	tgt	ggg	gga	aat	gaa	aac	aat		1018
Lys	Cys	Arg	Pro	Phe	Lys	Tyr	Ser	Gly	Cys	Gly	Gly	Asn	Glu	Asn	Asn		
				205				210					215				
ttt	act	tcc	aaa	caa	gaa	tgt	ctg	agg	gca	tgt	aaa	aaa	ggg	ttc	atc		1066
Phe	Thr	Ser	Lys	Gln	Glu	Cys	Leu	Arg	Ala	Cys	Lys	Lys	Gly	Phe	Ile		
			220					225					230				
caa	aga	ata	tca	aaa	gga	ggc	cta	att	aaa	acc	aaa	aga	aaa	aga	aag		1114
Gln	Arg	Ile	Ser	Lys	Gly	Gly	Leu	Ile	Lys	Thr	Lys	Arg	Lys	Arg	Lys		
	235					240						245					
aag	cag	aga	gtg	aaa	ata	gca	tat	gaa	gaa	att	ttt	gtt	aaa	aat	atg		1162
Lys	Gln	Arg	Val	Lys	Ile	Ala	Tyr	Glu	Glu	Ile	Phe	Val	Lys	Asn	Met		
	250				255						260						
tgaat	ttgtt	atagca	atgt	aacat	taatt	ctactaa	ata	ttttat	atga	aatgt	tttcac					1222	
tatga	ttttc	tattttt	ctt	ctaaa	atgct	tttaatta	at	atgttc	atta	aat	tttctat					1282	
gcttatt	gtga	cttgttat	ca	aaaaaaaa	aaaaa											1317	

<210> 52
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> 1..28

<400> 52

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      -25                      -20                      -15
Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu
      -10                      -5                      1
Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
5                      10                      15                      20
Leu Met His Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys
      25                      30                      35
Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
      40                      45                      50
Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
      55                      60                      65
Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys
      70                      75                      80
Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
85                      90                      95                      100
Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
      105                      110                      115
Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn
      120                      125                      130
Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr
      135                      140                      145
Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val
      150                      155                      160
Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala
165                      170                      175                      180
Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser
      185                      190                      195
Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn
      200                      205                      210
Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys
      215                      220                      225
Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg
      230                      235                      240
Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val
245                      250                      255                      260
Lys Asn Met
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<210> 53

<211> 1907

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..1043

<220>

<221> CDS

<222> 1044..1664

<220>

<221> 3'UTR

<222> 1665..1907

<220>

<221> polyA_signal

<222> 1869..1874

<220>

<221> polyA_site
 <222> 1892..1907

<400> 53

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cctggacatt	ttgggtattg	tttcagtggg	acatgccttt	cataagttcc	atcttcttgg	120
gtatctctta	ggaagcaagc	ataggaaaca	ggcccatccg	tctgcctgtt	ttgcttcctc	180
atctcacttc	tacacgaggg	tgccgtgtgt	caattgctgt	tttcccctaa	agagactctt	240
ttccataagt	ttgtgaaatg	ccatcgacaa	acctgatcgc	attgcatttc	actctgctgt	300
tgagtcgatt	tttctttatt	ttatcattta	gtaactcctt	gctctacaga	gctttcacct	360
tccacatatt	tcagattcat	tctttcctaa	actatgtggg	ggctctacgtc	ctcactgact	420
tatcaacatg	ctaccatcat	gcacttccta	tctctattcc	tcttctttaa	atcttggttcc	480
aaatggctca	caccattatt	ctgagctatt	acctgcctac	gcagtcctag	aaagtaagtg	540
attcaggaaa	cattcccaaa	aagtaaagtt	tctcaggtaa	gatcagaaga	ctcccatgag	600
tcactgctgc	tcaggatcac	atctggctcc	ttgaagagtg	attcatcaga	ccttacatag	660
atcttgtcat	aaaaatgaaa	gaggcctcgg	gggaaggctt	tgggctgggtg	gcttctgttg	720
gagtcctggg	ctgtgggggtg	aaagccgtgg	ctgtagagct	tcagtcggag	ttacttagct	780
ttgctctcct	gtggacaggc	catgcctgtg	cctcccccaa	gcacgcggaaa	aattggcata	840
gatggggcct	tctcaaaaat	cccactcctg	gagcactggc	caaaattact	accatcctga	900
tgctgggctt	gcagtccttt	cctttgggaa	tatgaacatg	gtcaaaaatta	agtgaacgtg	960
tctttctggc	tttctgtaca	atggagcaga	acaaagtatc	aatttaacta	aaatttgaac	1020
taaatcctct	ttccaggttt	gga atg cac ttc tgt gga ggc acc ttg ata tcc				1073
		Met His Phe Cys Gly Gly Thr Leu Ile Ser				
		1 5 10				
cca gag tgg gtg ttg act gct gcc cac tgc ttg gag aag tcc cca agg						1121
Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu Glu Lys Ser Pro Arg						
	15 20 25					
cct tca tcc tac aag gtc atc ctg ggt gca cac caa gaa gtg aat ctc						1169
Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln Glu Val Asn Leu						
	30 35 40					
gaa ccg cat gtt cag gaa ata gaa gtg tct agg ctg ttc ttg gag ccc						1217
Glu Pro His Val Gln Glu Ile Glu Val Ser Arg Leu Phe Leu Glu Pro						
	45 50 55					
aca cga aaa gat att gcc ttg cta aag cta agc agt cct gcc gtc atc						1265
Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser Ser Pro Ala Val Ile						
	60 65 70					
act gac aaa gta atc cca gct tgt ctg cca tcc cca aat tat gtg gtc						1313
Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser Pro Asn Tyr Val Val						
	75 80 85 90					
gct gac cgg acc gaa tgt ttc atc act ggc tgg gga gaa acc caa ggt						1361
Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly						
	95 100 105					
act ttt gga gct ggc ctt ctc aag gaa gcc cag ctc cct gtg att gag						1409
Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln Leu Pro Val Ile Glu						
	110 115 120					
aat aaa gtg tgc aat cgc tat gag ttt ctg aat gga aga gtc caa tcc						1457
Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser						
	125 130 135					
acc gaa ctc tgt gct ggg cat ttg gcc gga ggc act gac agt tgc cag						1505
Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr Asp Ser Cys Gln						
	140 145 150					
ggg gac agt gga ggt cct ctg gtt tgc ttc gag aag gac aaa tac att						1553
Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile						
	155 160 165 170					
tta caa gga gtc act tct tgg ggt ctt ggc tgt gca cgc ccc aat aag						1601
Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys						
	175 180 185					
cct ggt gtc tat gtt cgt gtt tca agg ttt gtt act tgg att gag gga						1649
Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr Trp Ile Glu Gly						
	190 195 200					
gtg atg aga aat aat taattggacg ggagacagag tgacgcactg actcacctag						1704
Val Met Arg Asn Asn						
205						


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aggctggaac gtgggtaggg atttagcatg ctggaaataa ctggcagtaa tcaaacgaag 1764
acactgtccc cagctaccag ctatgccaaa cctcggcatt ttttgtgtta ttttctgact 1824
gctggattct gtagtaaggt gacatagcta tgacatttgt taaaaataaa ctctgtactt 1884
aactttgaaa aaaaaaaaaa aaa
1907

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<210> 54
<211> 207
<212> PRT
<213> Homo sapiens

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<400> 54
Met His Phe Cys Gly Gly Thr Leu Ile Ser Pro Glu Trp Val Leu Thr
1      5      10      15
Ala Ala His Cys Leu Glu Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val
20     25     30
Ile Leu Gly Ala His Gln Glu Val Asn Leu Glu Pro His Val Gln Glu
35     40     45
Ile Glu Val Ser Arg Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala
50     55     60
Leu Leu Lys Leu Ser Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro
65     70     75     80
Ala Cys Leu Pro Ser Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys
85     90     95
Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu
100    105    110
Leu Lys Glu Ala Gln Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg
115    120    125
Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly
130    135    140
His Leu Ala Gly Gly Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
145    150    155    160
Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser
165    170    175
Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg
180    185    190
Val Ser Arg Phe Val Thr Trp Ile Glu Gly Val Met Arg Asn Asn
195    200    205

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<210> 55
<211> 809
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..25

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<220>
<221> CDS
<222> 26..628

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<220>
<221> 3'UTR
<222> 629..809

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<220>
<221> polyA_signal
<222> 766..771

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<220>
<221> polyA_site
<222> 795..809

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			Met	Leu	Glu	Val	Ser	Asp	Ala	Leu	Gly					
			1				5									
gga	cct	gga	aga	gta	cca	ggg	gcc	aca	gca	ggg	atg	aat	gga	gtg	gac	100
Gly	Pro	Gly	Arg	Val	Pro	Gly	Ala	Thr	Ala	Gly	Met	Asn	Gly	Val	Asp	
10					15					20					25	
acg	tcg	ctt	ctc	tgt	gat	ttg	ttg	cag	gcc	ctg	acc	ttc	ctg	acc	aga	148
Thr	Ser	Leu	Leu	Cys	Asp	Leu	Leu	Gln	Ala	Leu	Thr	Phe	Leu	Thr	Arg	
				30				35							40	
aat	gaa	att	ctg	tgc	atc	cat	gac	acc	ttc	ctg	aag	ctc	tgc	cct	cct	196
Asn	Glu	Ile	Leu	Cys	Ile	His	Asp	Thr	Phe	Leu	Lys	Leu	Cys	Pro	Pro	
			45					50						55		
ggg	aag	tac	tac	aag	gag	gca	acg	ctc	acc	atg	gac	cag	gtc	agc	tcc	244
Gly	Lys	Tyr	Tyr	Lys	Glu	Ala	Thr	Leu	Thr	Met	Asp	Gln	Val	Ser	Ser	
		60					65					70				
ctg	cca	gct	ctg	cgg	gtc	aac	cct	ttc	aga	gac	cgt	atc	tgc	aga	gtg	292
Leu	Pro	Ala	Leu	Arg	Val	Asn	Pro	Phe	Arg	Asp	Arg	Ile	Cys	Arg	Val	
		75				80					85					
ttc	tcc	cac	aaa	ggc	atg	ttc	tcc	ttt	gag	gat	gtg	ctg	ggc	atg	gca	340
Phe	Ser	His	Lys	Gly	Met	Phe	Ser	Phe	Glu	Asp	Val	Leu	Gly	Met	Ala	
90				95						100					105	
tct	gtg	ttc	agc	gag	cag	gcc	tgc	cca	agc	ctg	aag	att	gag	tat	gcc	388
Ser	Val	Phe	Ser	Glu	Gln	Ala	Cys	Pro	Ser	Leu	Lys	Ile	Glu	Tyr	Ala	
				110						115					120	
ttt	cgc	atc	tat	gat	ttt	aat	gag	aat	ggc	ttc	att	gat	gag	gag	gat	436
Phe	Arg	Ile	Tyr	Asp	Phe	Asn	Glu	Asn	Gly	Phe	Ile	Asp	Glu	Glu	Asp	
			125					130						135		
ctg	cag	agg	atc	atc	ctg	cga	ctg	ctg	aac	agt	gat	gac	atg	tct	gag	484
Leu	Gln	Arg	Ile	Ile	Leu	Arg	Leu	Leu	Asn	Ser	Asp	Asp	Met	Ser	Glu	
		140					145					150				
gac	ctc	ctg	atg	gac	ctc	acg	aac	cac	gtc	ctg	agt	gag	tcg	gat	ctg	532
Asp	Leu	Leu	Met	Asp	Leu	Thr	Asn	His	Val	Leu	Ser	Glu	Ser	Asp	Leu	
		155				160					165					
gac	aat	gac	aac	atg	ctg	tcc	ttc	tca	gag	ttt	gaa	cat	gca	atg	gcc	580
Asp	Asn	Asp	Asn	Met	Leu	Ser	Phe	Ser	Glu	Phe	Glu	His	Ala	Met	Ala	
170					175						180				185	
aag	tct	cca	gat	ttc	atg	aac	tcc	ttt	cgg	att	cac	ttc	tgg	gga	tgc	628
Lys	Ser	Pro	Asp	Phe	Met	Asn	Ser	Phe	Arg	Ile	His	Phe	Trp	Gly	Cys	
				190					195					200		
tgatgtagcg	gcaaatacct	gacatggcag	cctcgaggga	gaccacagga	atcgaacccc	688										
ctccagcact	ggagggagct	ggtttgaagt														

<210> 56

<211> 201

<212> PRT

<213> Homo sapiens

<400> 56

Met	Leu	Glu	Val	Ser	Asp	Ala	Leu	Gly	Gly	Pro	Gly	Arg	Val	Pro	Gly
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Ala	Thr	Ala	Gly	Met	Asn	Gly	Val	Asp	Thr	Ser	Leu	Leu	Cys	Asp	Leu
			20					25					30		
Leu	Gln	Ala	Leu	Thr	Phe	Leu	Thr	Arg	Asn	Glu	Ile	Leu	Cys	Ile	His
			35				40					45			
Asp	Thr	Phe	Leu	Lys	Leu	Cys	Pro	Pro	Gly	Lys	Tyr	Tyr	Lys	Glu	Ala
			50			55					60				
Thr	Leu	Thr	Met	Asp	Gln	Val	Ser	Ser	Leu	Pro	Ala	Leu	Arg	Val	Asn
65				70						75				80	
Pro	Phe	Arg	Asp	Arg	Ile	Cys	Arg	Val	Phe	Ser	His	Lys	Gly	Met	Phe
				85					90					95	

Ser Phe Glu Asp Val Leu Gly Met Ala Ser Val Phe Ser Glu Gln Ala
 100 105 110
 Cys Pro Ser Leu Lys Ile Glu Tyr Ala Phe Arg Ile Tyr Asp Phe Asn
 115 120 125
 Glu Asn Gly Phe Ile Asp Glu Asp Leu Gln Arg Ile Ile Leu Arg
 130 135 140
 Leu Leu Asn Ser Asp Asp Met Ser Glu Asp Leu Leu Met Asp Leu Thr
 145 150 155 160
 Asn His Val Leu Ser Glu Ser Asp Leu Asp Asn Asp Asn Met Leu Ser
 165 170 175
 Phe Ser Glu Phe Glu His Ala Met Ala Lys Ser Pro Asp Phe Met Asn
 180 185 190
 Ser Phe Arg Ile His Phe Trp Gly Cys
 195 200

<210> 57
 <211> 1133
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..475

<220>
 <221> CDS
 <222> 476..964

<220>
 <221> 3'UTR
 <222> 965..1133

<220>
 <221> polyA_signal
 <222> 1101..1106

<220>
 <221> polyA_site
 <222> 1118..1133

<400> 57
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 gagccaggag gtggcaggac gagttaggag gctgggttcag tagctcgggc aagagcaggg 120
 cccccagga tctgaaggcc tcccaggccc cccaggccca gcgggtccca gaggagagcg 180
 aggaccccaa ggtaactccg gtgagaaggg cgaccaggga tttcaaggcc agccaggctt 240
 tccgggcca ccgggtcccc ctggattccc aggcaaagtt ggatcacctg gccacactgg 300
 ccctcaagca gagaaggcca gcgaagggat tcgaggccca tcaggcctgc ctggctcccc 360
 tgggccaccg ggacctcctg ggattcaggg ccccgccggg ctggatgggt tggatgggaa 420
 ggatggcaag cctggcttga ggggggaccc tggtcctgct ggccccctg gactc atg 478
 Met
 1
 gga cca ccg ggc ttt aag ggg aaa aca gga cat cct ggc ctc cca gga 526
 Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro Gly
 5 10 15
 cct aag ggt gac tgt ggc aaa cca ggt cct cct ggc agc act ggc cgg 574
 Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly Arg
 20 25 30
 cct ggc gca gag ggt gaa cct ggt gcc atg gga ccc cag gga aga ccc 622
 Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg Pro
 35 40 45
 ggt ccc ccg gga cac gtt ggg cca cca ggg cct cca ggc cag cca gga 670
 Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Gly Gln Pro Gly
 50 55 60 65

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cca gct ggg atc tct gca gtg ggt ctg aaa gga gac cga gga gcc acc 718
Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala Thr
      70      75      80
gga gaa agg ggc ctt gca ggc ctc cca ggc cag ccc ggc ccc cca ggt 766
Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro Gly
      85      90      95
cct caa ggt cct cca ggc tat ggc aag atg ggt gca aca gga cca atg 814
Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro Met
      100      105      110
ggc cag caa ggc atc cct ggc atc cct ggg ccc ccg ggt ccc atg ggc 862
Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met Gly
      115      120      125
cag cca ggc aag gct ggc cac tgt aat ccc tct gac tgc ttt ggg gcc 910
Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly Ala
      130      135      140      145
atg ccg atg gag cag cag tac cca ccc atg aaa acc atg aag ggg cct 958
Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly Pro
      150      155      160
ttt ggc tgaaattccc cacctgcctt tggatgaaag actccgttgg gaataaatgg 1014
Phe Gly
ccaaagctta taggactctg tgacagggttg tgaatgtttt ttttgttggt gttgttggtt 1074
ttaattgctg ttaatatattt ttaaataata aagaaacaaa actaaaaaaaa aaaaaaaaaa 1133

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<210> 58
<211> 163
<212> PRT
<213> Homo sapiens

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<400> 58
Met Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro
1      5      10      15
Gly Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly
      20      25      30
Arg Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg
      35      40      45
Pro Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro
      50      55      60
Gly Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala
65      70      75      80
Thr Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro
      85      90      95
Gly Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro
      100      105      110
Met Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met
      115      120      125
Gly Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly
      130      135      140
Ala Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly
145      150      155      160
Pro Phe Gly

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<210> 59
<211> 838
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..78

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<220>
<221> CDS
<222> 79..642

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<220>
 <221> 3'UTR
 <222> 643..838

<220>
 <221> polyA_signal
 <222> 799..804

<220>
 <221> polyA_site
 <222> 823..838

<400> 59
 aaagactgcg tgcagaaggt gactgtctca gtggagctgg gtcattctcag gccttggctc 60
 cttgaacttt tggccgcc atg tgc ttc ccg aag gtc ctc tct gat gac atg 111
 Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met
 1 5 10
 aag aag ctg aag gcc cga atg cac cag gcc ata gaa aga ttt tat gat 159
 Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp
 15 20 25
 aaa atg caa aat gca gaa tca gga cgt gga cag gtg atg tcg agc ctg 207
 Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu
 30 35 40
 gca gag ctg gag gac gac ttc aaa gag ggc tac ctg gag aca gtg gcg 255
 Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala
 45 50 55
 gct tat tat gag gag cag cac cca gag ctc act cct cta ctt gaa aaa 303
 Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys
 60 65 70 75
 gaa aga gat gga tta cgg tgc cga ggc aac aga tcc cct gtc ccg gat 351
 Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp
 80 85 90
 gtt gag gat ccc gca acc gag gag cct ggg gag agc ttt tgt gac aag 399
 Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys
 95 100 105
 gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg cag acc tgg tgg 447
 Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp
 110 115 120
 cac ggg gtt ctg gcc tgg gtg aag gag aag gtg gtg gcc ctg gtc cat 495
 His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val Ala Leu Val His
 125 130 135
 gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc tgc tgc tct ctg 543
 Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu
 140 145 150 155
 tca gag ctc ttc atg tcc tct ttc cag tcc tac gga gcc cca cgg ggg 591
 Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly
 160 165 170
 gac aag gag gag ctg aca ccc cag aag tgc tct gaa ccc caa tcc tca 639
 Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser
 175 180 185
 aaa tgaagatact gacaccacct ttgccctccc cgtcaccgcg caccacacct 692
 Lys
 gaccctccc tcagctgtcc tgtgccccgc cctctcccgc acactcagtc cccctgcctg 752
 gcgttcctgc cgcagctctg acctggtgct gtgcacctgg catcttaata aamcctgctt 812
 atacttcctt aaaaaaaaaa aaaaaa 838

<210> 60
 <211> 188
 <212> PRT
 <213> Homo sapiens

<400> 60

Met	Cys	Phe	Pro	Lys	Val	Leu	Ser	Asp	Asp	Met	Lys	Lys	Leu	Lys	Ala	
1				5					10					15		
Arg	Met	His	Gln	Ala	Ile	Glu	Arg	Phe	Tyr	Asp	Lys	Met	Gln	Asn	Ala	
			20					25					30			
Glu	Ser	Gly	Arg	Gly	Gln	Val	Met	Ser	Ser	Leu	Ala	Glu	Leu	Glu	Asp	
		35					40					45				
Asp	Phe	Lys	Glu	Gly	Tyr	Leu	Glu	Thr	Val	Ala	Ala	Tyr	Tyr	Glu	Glu	
	50					55					60					
Gln	His	Pro	Glu	Leu	Thr	Pro	Leu	Leu	Glu	Lys	Glu	Arg	Asp	Gly	Leu	
65					70					75					80	
Arg	Cys	Arg	Gly	Asn	Arg	Ser	Pro	Val	Pro	Asp	Val	Glu	Asp	Pro	Ala	
				85					90					95		
Thr	Glu	Glu	Pro	Gly	Glu	Ser	Phe	Cys	Asp	Lys	Val	Met	Arg	Trp	Phe	
			100					105						110		
Gln	Ala	Met	Leu	Gln	Arg	Leu	Gln	Thr	Trp	Trp	His	Gly	Val	Leu	Ala	
		115					120					125				
Trp	Val	Lys	Glu	Lys	Val	Val	Ala	Leu	Val	His	Ala	Val	Gln	Ala	Leu	
	130					135					140					
Trp	Lys	Gln	Phe	Gln	Ser	Phe	Cys	Cys	Ser	Leu	Ser	Glu	Leu	Phe	Met	
145					150					155					160	
Ser	Ser	Phe	Gln	Ser	Tyr	Gly	Ala	Pro	Arg	Gly	Asp	Lys	Glu	Glu	Leu	
				165					170						175	
Thr	Pro	Gln	Lys	Cys	Ser	Glu	Pro	Gln	Ser	Ser	Lys					
			180					185								

<210> 61
 <211> 862
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..158

<220>
 <221> CDS
 <222> 159..764

<220>
 <221> 3'UTR
 <222> 765..862

<400> 61
 attttttttt ttggcacgcc tgcagccaag ttggggaggg tttcctggac agaggtcctt 60
 tggtctgtgc cttaagacgt gcagcctggg ccgtggctgt cactgcgttc ggaccagac 120
 ccgctgcagg cagcagcagc ccccgccgc gcagcagc atg gag ctc tgg ggg gcc 176
 Met Glu Leu Trp Gly Ala
 -20 -15
 tac ctc ctc ctc tgc ctc ttc tcc ctc ctg acc cag gtc acc acc gag 224
 Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu Thr Gln Val Thr Thr Glu
 -10 -5 1
 cca cca acc cag aag ccc aag aag att gta aat gcc aag aaa gat gtt 272
 Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp Val
 5 10 15
 gtg aac aca aag atg ttt gag gag ctc aag agc cgt ctg gac acc ctg 320
 Val Asn Thr Lys Met Phe Glu Leu Lys Ser Arg Leu Asp Thr Leu
 20 25 30
 gcc cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg cag acg gtc 368
 Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val
 35 40 45 50
 tgc ctg aag ggg acc aag gtg cac atg aaa tgc ttt ctg gcc ttc acc 416
 Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe Thr
 55 60 65

```

cag acg aag acc ttc cac gag tcc agc gag gac tgc atc tcg cgc ggg 464
Gln Thr Lys Thr Phe His Glu Ser Ser Glu Asp Cys Ile Ser Arg Gly
70 75 80
ggc acc ctg agc acc cct cag act ggc tcg gag aac gac gcc ctg tat 512
Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu Tyr
85 90 95
gag tac ctg cgc cag agc gtg ggc aac gag gcc gag atc tgg ctg ggc 560
Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu Gly
100 105 110
ctc aac gac atg gcg gcc gag ggc acc tgg gtg gac atg acc ggc gcc 608
Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly Ala
115 120 125 130
cgc atc gcc tac aag aac tgg gag act gag atc acc gcg caa ccc gat 656
Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp
135 140 145
ggc ggc aag acc gag aac tgc gcg gtc ctg tca ggc gcg gcc aac ggc 704
Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly
150 155 160
aag tgg ttc gac aag cgc tgc cgc gat cag ctg ccc tac atc tgc cag 752
Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln
165 170 175
ttc ggg atc gtg tagccggcgg ggcgggggcc gtgggggggcc tggaggaggg 804
Phe Gly Ile Val
180
caggagccgc gggaggccgg gaggaggggtg gggaccttgc agcccccatc ctctccgt 862

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<210> 62

<211> 202

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..21

<400> 62

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Met Glu Leu Trp Gly Ala Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu
-20 -15 -10
Thr Gln Val Thr Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val
-5 1 5 10
Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys
15 20 25
Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln
30 35 40
Gln Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys
45 50 55
Cys Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ser Ser Glu
60 65 70 75
Asp Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser
80 85 90
Glu Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu
95 100 105
Ala Glu Ile Trp Leu Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp
110 115 120
Val Asp Met Thr Gly Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu
125 130 135
Ile Thr Ala Gln Pro Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu
140 145 150 155
Ser Gly Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln
160 165 170
Leu Pro Tyr Ile Cys Gln Phe Gly Ile Val
175 180

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<210> 63
 <211> 618
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..194

<220>
 <221> CDS
 <222> 195..587

<220>
 <221> 3'UTR
 <222> 588..618

<220>
 <221> polyA_signal
 <222> 578..583

<220>
 <221> polyA_site
 <222> 604..618

<400> 63
 atttgcttag gtctgatcaa tctgctccac acaatttctc agtgatcctc tgcattctctg 60
 cctacaaggg cctccctgac acccaagttc atattgctca gaaacagtga acttgagttt 120
 ttcgtttttac cttgatctct ctctgacaaa gaaatccaga tgatgcgaga cctgatgaag 180
 acaatacatg gaaa atg aca gtc ttg gaa ata act ttg gct gtc atc ctg 230
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu
 -20 -15 -10
 act cta ctg gga ctt gcc atc ctg gct att ttg tta aca aga tgg gca 278
 Thr Leu Leu Gly Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala
 -5 1 5
 cga cgt aag caa agt gaa atg cat atc tcc aga tac agt tca gaa caa 326
 Arg Arg Lys Gln Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln
 10 15 20
 agt gct aga ctt ctg gac tat gag gat ggt aga gga tcc cga cat gca 374
 Ser Ala Arg Leu Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala
 25 30 35
 tat tca aca caa agt gag aga tcc aaa aga gat tac aca cca tca acc 422
 Tyr Ser Thr Gln Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr
 40 45 50 55
 aac tct cta gca ctg tct cga tca agt att gct tta cct caa gga tcc 470
 Asn Ser Leu Ala Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser
 60 65 70
 atg agt agt ata aaa tgt tta caa aca act gaa gaa ctt cct tcc aga 518
 Met Ser Ser Ile Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg
 75 80 85
 act gca gga gcc atg agt aag ttc ttt ttc tgc cct tta att ctc atg 566
 Thr Ala Gly Ala Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met
 90 95 100
 tgc ttt gct tta cta aac tgt tagaatatgt aagacgaaaa aaaaaaaaaa a 618
 Cys Phe Ala Leu Leu Asn Cys
 105 110

<210> 64
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..22

<400> 64

Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly
-20 -15 -10
Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
-5 1 5 10
Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
15 20 25
Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
30 35 40
Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala
45 50 55
Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile
60 65 70
Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg Thr Ala Gly Ala
75 80 85 90
Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met Cys Phe Ala Leu
95 100 105
Leu Asn Cys

<210> 65

<211> 836

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..176

<220>

<221> CDS

<222> 177..767

<220>

<221> 3'UTR

<222> 768..836

<220>

<221> polyA_signal

<222> 814..819

<220>

<221> polyA_site

<222> 822..836

<400> 65

aatctgctcc acgcaatttc tcagtgatcc tctgcatctc tgccatacaag ggcctccctg 60
acacccaagt tcatattgct cagaaacagt gaacttgagt ttttcatttt accttgatct 120
ctctctgaca aagaaatcca gatgatgcga gacctgatga agacaatata tggaaa atg 179
Met
aca gtc ttg gaa ata act ttg gct gtc atc ctg act cta ctg gga ctt 227
Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly Leu
-20 -15 -10 -5
gcc atc ctg gct att ttg tta aca aga tgg gca cga cgt aag caa agt 275
Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln Ser
1 5 10
gaa atg tat atc tcc aga tac agt tca gaa caa agt gct aga ctt ctg 323
Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu Leu
15 20 25
gac tat gag gat ggt aga gga tcc cga cat gca tat tca aca caa agt 371
Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln Ser

30	35	40	
gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg			419
Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu			
45	50	55	60
tct cga tca agt att gct tta cct caa gga tcc atg agt agt ata aaa			467
Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys			
65	70	75	
tgt tta caa aca act gaa gaa cct cct tcc aga act gca gga gcc atg			515
Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met			
80	85	90	
atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc			563
Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu			
95	100	105	
tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct			611
Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro			
110	115	120	
gga tcc aat ggg agg ata aac ata agc cag ctc acc tca gag gat ctc			659
Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu			
125	130	135	140
act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc			707
Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser			
145	150	155	
cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt			755
His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu			
160	165	170	
ttc tcc cct gct tgactccctc tcccttatgt gtaaacaatt taaaaaatatg			807
Phe Ser Pro Ala			
175			
atagtgtata aatgaaaaaaaa aaaaaaaaaa			836

<210> 66

<211> 197

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..22

<400> 66

Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly	
-20	-15
Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln	
-5	1
Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu	10
15	20
Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln	25
30	35
Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala	40
45	50
Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile	55
60	65
Lys Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala	70
75	80
Met Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys	85
95	100
Leu Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr	105
110	115
Pro Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp	120
125	130
Leu Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn	135
140	145
Ser His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser	150

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155          160          165          170
Leu Phe Ser Pro Ala
          175

<210> 67
<211> 789
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..62

<220>
<221> CDS
<222> 63..572

<220>
<221> 3'UTR
<222> 573..789

<220>
<221> polyA_signal
<222> 750..755

<220>
<221> polyA_site
<222> 774..789

<400> 67
atatgtcatc aggccccccg cctgggaggt gtgctgccag agattttgcc tcttcaaggt 60
ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
1 5 10 15
ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
20 25 30
gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
35 40 45
ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
50 55 60
gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
65 70 75
ctt cgc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
Leu Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
80 85 90 95
ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
100 105 110
ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
115 120 125
aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
130 135 140
gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
Val Thr Ser Ala Leu Thr His Leu Trp Arg Asp Ser Leu Cys Pro
145 150 155
gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp

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160          165          170
gaggaggggac gccacgggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggtt 652
caccccaatg ggaccaccct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712
aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaactcc 772
gaaaaaaaaa aaaaaaa                                789

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<210> 68
<211> 170
<212> PRT
<213> Homo sapiens

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<400> 68
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro
1          5          10          15
Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
20         25         30
Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
35         40         45
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
50         55         60
Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
65         70         75         80
Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
85         90         95
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
100        105        110
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
115        120        125
Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
130        135        140
Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
145        150        155        160
His Gln Pro Gln Pro Thr Glu Lys Ser Asp
165        170

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<210> 69
<211> 2556
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..66

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<220>
<221> CDS
<222> 67..2427

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<220>
<221> 3'UTR
<222> 2428..2556

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<220>
<221> polyA_signal
<222> 2522..2527

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<220>
<221> polyA_site
<222> 2541..2556

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<400> 69
gtccccgcgt ccctggcaat tcccgaacttc ccaacgggtt cctgctggca gccccgaagc 60
cgcacc atg ttc cgc ctc tgg ttg ctg ctg gcc ggg ctc tgc ggc ctc 108

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	Met	Phe	Arg	Leu	Trp	Leu	Leu	Leu	Ala	Gly	Leu	Cys	Gly	Leu		
	-15					-10					-5					
ctg	gcg	tca	aga	ccc	ggg	ttt	caa	aat	tca	ctt	cta	cag	atc	gta	att	156
Leu	Ala	Ser	Arg	Pro	Gly	Phe	Gln	Asn	Ser	Leu	Leu	Gln	Ile	Val	Ile	
1					5					10				15		
cca	gag	aaa	atc	caa	aca	aat	aca	aat	gac	agt	tca	gaa	ata	gaa	tat	204
Pro	Glu	Lys	Ile	Gln	Thr	Asn	Thr	Asn	Asp	Ser	Ser	Glu	Ile	Glu	Tyr	
				20					25					30		
gaa	caa	ata	tcc	tat	att	att	cca	ata	gat	gag	aaa	ctg	tac	act	gtg	252
Glu	Gln	Ile	Ser	Tyr	Ile	Ile	Pro	Ile	Asp	Glu	Lys	Leu	Tyr	Thr	Val	
			35						40					45		
cac	ctt	aaa	caa	aga	tat	ttt	tta	aca	gat	aat	ttt	atg	atc	tat	ttg	300
His	Leu	Lys	Gln	Arg	Tyr	Phe	Leu	Thr	Asp	Asn	Phe	Met	Ile	Tyr	Leu	
		50					55					60				
tac	aat	caa	gga	tct	atg	aat	act	tat	tct	tca	gat	att	cag	act	caa	348
Tyr	Asn	Gln	Gly	Ser	Met	Asn	Thr	Tyr	Ser	Ser	Asp	Ile	Gln	Thr	Gln	
	65					70										
tgc	tac	tat	caa	gga	aat	att	gaa	gaa	tat	cca	gat	tcc	atg	gtc	aca	396
Cys	Tyr	Tyr	Gln	Gly	Asn	Ile	Glu	Glu	Tyr	Pro	Asp	Ser	Met	Val	Thr	
80					85					90				95		
ctc	agc	acg	tgc	tct	gga	cta	aga	gga	ata	ctg	caa	ttt	gaa	aat	gtt	444
Leu	Ser	Thr	Cys	Ser	Gly	Leu	Arg	Gly	Ile	Leu	Gln	Phe	Glu	Asn	Val	
				100					105					110		
tct	tat	gga	att	gag	cct	ctg	gaa	tct	gca	gtt	gaa	ttt	cag	cat	gtt	492
Ser	Tyr	Gly	Ile	Glu	Pro	Leu	Glu	Ser	Ala	Val	Glu	Phe	Gln	His	Val	
		115						120					125			
ctt	cac	aaa	tta	aag	aat	gaa	gac	aat	gat	att	gca	att	ttt	att	gac	540
Leu	His	Lys	Leu	Lys	Asn	Glu	Asp	Asn	Asp	Ile	Ala	Ile	Phe	Ile	Asp	
		130					135					140				
aga	agc	ctg	aaa	gaa	caa	cca	atg	gat	gac	aac	att	ttt	ata	agt	gaa	588
Arg	Ser	Leu	Lys	Glu	Gln	Pro	Met	Asp	Asp	Asn	Ile	Phe	Ile	Ser	Glu	
		145				150					155					
aaa	tca	gaa	cca	gct	gtt	cca	gat	tta	ttt	cct	ctt	tat	cta	gaa	atg	636
Lys	Ser	Glu	Pro	Ala	Val	Pro	Asp	Leu	Phe	Pro	Leu	Tyr	Leu	Glu	Met	
160					165					170				175		
cat	att	gtg	gtg	gac	aaa	act	ttg	tat	gat	tac	tgg	ggc	tct	gat	agc	684
His	Ile	Val	Val	Asp	Lys	Thr	Leu	Tyr	Asp	Tyr	Trp	Gly	Ser	Asp	Ser	
				180					185					190		
atg	ata	gta	aca	aat	aaa	gtc	atc	gaa	att	gtt	ggc	ctt	gca	aat	tca	732
Met	Ile	Val	Thr	Asn	Lys	Val	Ile	Glu	Ile	Val	Gly	Leu	Ala	Asn	Ser	
				195				200					205			
atg	ttc	acc	caa	ttt	aaa	gtt	act	att	gtg	ctg	tca	tca	ttg	gag	tta	780
Met	Phe	Thr	Gln	Phe	Lys	Val	Thr	Ile	Val	Leu	Ser	Ser	Leu	Glu	Leu	
		210					215					220				
tgg	tca	gat	gaa	aat	aag	att	tct	aca	gtt	ggg	gag	gca	gat	gaa	tta	828
Trp	Ser	Asp	Glu	Asn	Lys	Ile	Ser	Thr	Val	Gly	Glu	Ala	Asp	Glu	Leu	
		225				230					235					
ttg	caa	aaa	ttt	tta	gaa	tgg	aaa	caa	tct	tat	ctt	aac	cta	agg	cct	876
Leu	Gln	Lys	Phe	Leu	Glu	Trp	Lys	Gln	Ser	Tyr	Leu	Asn	Leu	Arg	Pro	
240					245					250				255		
cat	gat	att	gca	tat	cta	cta	att	tat	atg	gat	tat	cct	cgt	tat	ttg	924
His	Asp	Ile	Ala	Tyr	Leu	Leu	Ile	Tyr	Met	Asp	Tyr	Pro	Arg	Tyr	Leu	
				260				265						270		
gga	gca	gtg	ttt	cct	gga	aca	atg	tgt	att	act	cgt	tat	tct	gca	gga	972
Gly	Ala	Val	Phe	Pro	Gly	Thr	Met	Cys	Ile	Thr	Arg	Tyr	Ser	Ala	Gly	
			275				280						285			
gtc	gca	ttg	tac	ccc	aag	gag	ata	act	ctg	gag	gca	ttt	gca	gtt	att	1020
Val	Ala	Leu	Tyr	Pro	Lys	Glu	Ile	Thr	Leu	Glu	Ala	Phe	Ala	Val	Ile	
		290					295					300				
gtc	acc	cag	atg	ctg	gca	ctc	agt	ctg	gga	ata	tca	tat	gac	gac	cca	1068
Val	Thr	Gln	Met	Leu	Ala	Leu	Ser	Leu	Gly	Ile	Ser	Tyr	Asp	Asp	Pro	
		305				310					315					
aag	aaa	tgt	caa	tgt	tca	gaa	tcc	acc	tgt	ata	atg	aat	cca	gaa	gtt	1116

Lys	Lys	Cys	Gln	Cys	Ser	Glu	Ser	Thr	Cys	Ile	Met	Asn	Pro	Glu	Val	
320					325					330					335	
gtg	caa	tcc	aat	ggg	gtg	aag	act	ttt	agc	agt	tgc	agt	ttg	agg	agc	1164
Val	Gln	Ser	Asn	Gly	Val	Lys	Thr	Phe	Ser	Ser	Cys	Ser	Leu	Arg	Ser	
				340					345					350		
ttt	caa	aat	ttc	att	tca	aat	gtg	ggg	gtc	aaa	tgt	ctt	cag	aat	aag	1212
Phe	Gln	Asn	Phe	Ile	Ser	Asn	Val	Gly	Val	Lys	Cys	Leu	Gln	Asn	Lys	
			355					360					365			
cca	caa	atg	caa	aaa	aaa	tct	ccg	aaa	cca	gtc	tgt	ggc	aat	ggc	aga	1260
Pro	Gln	Met	Gln	Lys	Lys	Ser	Pro	Lys	Pro	Val	Cys	Gly	Asn	Gly	Arg	
		370					375					380				
ttg	gag	gga	aat	gaa	atc	tgt	gat	tgt	ggg	act	gag	gct	caa	tgt	gga	1308
Leu	Glu	Gly	Asn	Glu	Ile	Cys	Asp	Cys	Gly	Thr	Glu	Ala	Gln	Cys	Gly	
	385					390				395						
cct	gca	agc	tgt	tgt	gat	ttt	cga	act	tgt	gta	ctg	aaa	gac	gga	gca	1356
Pro	Ala	Ser	Cys	Cys	Asp	Phe	Arg	Thr	Cys	Val	Leu	Lys	Asp	Gly	Ala	
400					405					410					415	
aaa	tgt	tat	aaa	gga	ctg	tgc	tgc	aaa	gac	tgt	caa	att	tta	caa	tca	1404
Lys	Cys	Tyr	Lys	Gly	Leu	Cys	Cys	Lys	Asp	Cys	Gln	Ile	Leu	Gln	Ser	
			420						425				430			
ggc	gtt	gaa	tgt	agg	ccg	aaa	gca	cat	cct	gaa	tgt	gac	atc	gct	gaa	1452
Gly	Val	Glu	Cys	Arg	Pro	Lys	Ala	His	Pro	Glu	Cys	Asp	Ile	Ala	Glu	
		435						440					445			
aat	tgt	aat	gga	agc	tca	cca	gaa	tgt	ggg	cct	gac	ata	act	tta	atc	1500
Asn	Cys	Asn	Gly	Ser	Ser	Pro	Glu	Cys	Gly	Pro	Asp	Ile	Thr	Leu	Ile	
	450						455				460					
aat	gga	ctt	tca	tgc	aaa	aat	aat	aag	ttt	att	tgt	tat	gac	gga	gac	1548
Asn	Gly	Leu	Ser	Cys	Lys	Asn	Asn	Lys	Phe	Ile	Cys	Tyr	Asp	Gly	Asp	
	465				470				475							
tgc	cat	gat	ctc	gat	gca	cgt	tgt	gag	agt	gta	ttt	gga	aaa	ggg	tca	1596
Cys	His	Asp	Leu	Asp	Ala	Arg	Cys	Glu	Ser	Val	Phe	Gly	Lys	Gly	Ser	
480					485					490				495		
aga	aat	gct	cca	ttt	gcc	tgc	tat	gaa	gaa	ata	caa	tct	caa	tca	gac	1644
Arg	Asn	Ala	Pro	Phe	Ala	Cys	Tyr	Glu	Glu	Ile	Gln	Ser	Gln	Ser	Asp	
			500						505				510			
aga	ttt	ggg	aac	tgt	ggg	agg	gat	aga	aat	aac	aaa	tat	gtg	ttc	tgt	1692
Arg	Phe	Gly	Asn	Cys	Gly	Arg	Asp	Arg	Asn	Asn	Lys	Tyr	Val	Phe	Cys	
		515					520						525			
gga	tgg	agg	aat	ctt	ata	tgt	gga	aga	tta	gtt	tgt	acc	tac	cct	act	1740
Gly	Trp	Arg	Asn	Leu	Ile	Cys	Gly	Arg	Leu	Val	Cys	Thr	Tyr	Pro	Thr	
	530					535					540					
cga	aag	cct	ttc	cat	caa	gaa	aat	ggg	gat	gtg	att	tat	gct	ttc	gta	1788
Arg	Lys	Pro	Phe	His	Gln	Glu	Asn	Gly	Asp	Val	Ile	Tyr	Ala	Phe	Val	
	545				550					555						
cga	gat	tct	gta	tgc	ata	acc	gta	gac	tac	aaa	ttg	cct	cga	aca	gtt	1836
Arg	Asp	Ser	Val	Cys	Ile	Thr	Val	Asp	Tyr	Lys	Leu	Pro	Arg	Thr	Val	
560				565					570					575		
cca	gat	cca	ctg	gct	gtc	aaa	aat	ggc	tct	cag	tgt	gat	att	ggg	agg	1884
Pro	Asp	Pro	Leu	Ala	Val	Lys	Asn	Gly	Ser	Gln	Cys	Asp	Ile	Gly	Arg	
			580					585					590			
gtt	tgt	gta	aat	cgt	gaa	tgt	gta	gaa	tca	agg	ata	att	aag	gct	tca	1932
Val	Cys	Val	Asn	Arg	Glu	Cys	Val	Glu	Ser	Arg	Ile	Ile	Lys	Ala	Ser	
		595				600						605				
gca	cat	gtt	tgt	tca	caa	cag	tgt	tct	gga	cat	gga	gtg	tgt	gat	tcc	1980
Ala	His	Val	Cys	Ser	Gln	Gln	Cys	Ser	Gly	His	Gly	Val	Cys	Asp	Ser	
	610					615					620					
aga	aac	aag	tgc	cat	tgt	tcg	cca	ggc	tat	aag	cct	cca	aac	tgc	caa	2028
Arg	Asn	Lys	Cys	His	Cys	Ser	Pro	Gly	Tyr	Lys	Pro	Pro	Asn	Cys	Gln	
	625				630					635						
ata	cgt	tcc	aaa	gga	ttt	tcc	ata	ttt	cct	gag	gaa	gat	atg	ggg	tca	2076
Ile	Arg	Ser	Lys	Gly	Phe	Ser	Ile	Phe	Pro	Glu	Glu	Asp	Met	Gly	Ser	
640				645					650					655		
atc	atg	gaa	aga	gca	tct	ggg	aag	act	gaa	aac	acc	tgg	ctt	cta	ggg	2124

Ile Met Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr Trp Leu Leu Gly	
660	665
670	670
ttc ctc att gct ctt cct att ctc att gta aca acc gca ata gtt ttg	2172
Phe Leu Ile Ala Leu Pro Ile Leu Ile Val Thr Thr Ala Ile Val Leu	
675	680
685	
gca agg aaa cag ttg aaa aac tgg ttc gcc aag gaa gag gaa ttc cca	2220
Ala Arg Lys Gln Leu Lys Asn Trp Phe Ala Lys Glu Glu Glu Phe Pro	
690	695
700	
agt agc gaa tct aaa tcg gaa ggt agc aca cag aca tat gcc agc caa	2268
Ser Ser Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln	
705	710
715	
tcc agc tca gaa ggc agc act cag aca tat gcc ggc caa acc aga tca	2316
Ser Ser Ser Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser	
720	725
730	735
gaa agc agc agt caa gct gat act agc aaa tcc aaa tca gaa gat agt	2364
Glu Ser Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser	
740	745
750	
gct gaa gca tat act agc aga tcc aaa tca cag gac agt acc caa aca	2412
Ala Glu Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr	
755	760
765	
caa agc agt agt aac tagtgattcc ttcagaaggc aacggataac atcgagagtc	2467
Gln Ser Ser Ser Asn	
770	
tcgctaagaa atgaaaattc tgtcttttcc tccgtgggtca cagctgaaag aaacaataaa	2527
ttgagtgtgg accaaaaaaaaa aaaaaaaaaat	2556

<210> 70

<211> 787

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..16

<400> 70

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1	5
10	15
Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln	
20	25
30	
Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu	
35	40
45	
Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu Tyr Asn	
50	55
60	
Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr	
65	70
75	80
Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr Leu Ser	
85	90
95	
Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr	
100	105
110	
Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu His	
115	120
125	
Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser	
130	135
140	
Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Ser	
145	150
155	160
Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met His Ile	
165	170
175	
Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser Met Ile	
180	185
190	
Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser Met Phe	

Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln Ser Ser
 705 710 715 720
 Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser Glu Ser
 725 730 735
 Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser Ala Glu
 740 745 750
 Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr Gln Ser
 755 760 765
 Ser Ser Asn
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<210> 71
 <211> 1603
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..7

<220>
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 <222> 8..763

<220>
 <221> 3'UTR
 <222> 764..1603

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 <222> 1562..1567

<220>
 <221> polyA_site
 <222> 1588..1603

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 <221> UNSURE
 <222> 157
 <223> Xaa = Ala,Gly

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 -15 -10 -5
 cgg tca ctc cgt gtc tgt gtg tcc ctc tgg tct gtc cac cac agg cca 97
 Arg Ser Leu Arg Val Cys Val Ser Leu Trp Ser Val His His Arg Pro
 1 5 10
 cac gag tcc ctg gcc cgg gag gag gcc ctc act gca ctt ggg aag ctc 145
 His Glu Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu
 15 20 25 30
 ctg tac ctc tta gat ggg atg ctg gat ggg cag gtg aac agt ggt ata 193
 Leu Tyr Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile
 35 40 45
 gca gcc act cca gcc tct gct gca gca gcc acc ctg gat gtg gct gtt 241
 Ala Ala Thr Pro Ala Ser Ala Ala Ala Thr Leu Asp Val Ala Val
 50 55 60
 cgg aga ggc ctg tcc cac gca gcc cag agg ctg ctg tgc gtg gcc ctg 289
 Arg Arg Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu
 65 70 75
 gga cag ctg gac cgg cct cca gac ctc gcc cat gac ggg agg agt ctg 337
 Gly Gln Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu
 80 85 90

tgg ctg aac atc agg ggc aag gag gcg gct gcc cta tcc atg ttc cat	385
Trp Leu Asn Ile Arg Gly Lys Glu Ala Ala Leu Ser Met Phe His	
95 100 105 110	
gtc tcc acg cca ctg cca gtg atg acc ggt ttc ctg agc tgc atc	433
Val Ser Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile	
115 120 125	
ttg ggc ttg gtg ctg ccc ctg gcc tat ggc ttc cag cct gac ctg gtg	481
Leu Gly Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val	
130 135 140	
ctg gtg gcg ctg ggg cct ggc cat ggc ctg cag ggc ccc cac gst gca	529
Leu Val Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Xaa Ala	
145 150 155	
ctc ctg gct gca atg ctt cgg ggg ctg gca ggg ggc cga gtc ctg gcc	577
Leu Leu Ala Ala Met Leu Arg Gly Leu Ala Gly Arg Val Leu Ala	
160 165 170	
ctc ctg gag gag aac tcc aca ccc cag cta gca ggg atc ctg gcc cgg	625
Leu Leu Glu Glu Asn Ser Thr Pro Gln Leu Ala Gly Ile Leu Ala Arg	
175 180 185 190	
gtg ctg aat gga gag gca cct cct agc cta ggc cct tcc tct gtg gcc	673
Val Leu Asn Gly Glu Ala Pro Pro Ser Leu Gly Pro Ser Ser Val Ala	
195 200 205	
tcc cca gag gac gtc cag gcc ctg atg tac ctg aga ggg cag ctg gag	721
Ser Pro Glu Asp Val Gln Ala Leu Met Tyr Leu Arg Gly Gln Leu Glu	
210 215 220	
cct cag tgg aag atg ttg cag tgc cat cct cac ctg gtg gct	763
Pro Gln Trp Lys Met Leu Gln Cys His Pro His Leu Val Ala	
225 230 235	
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gcggccgcga tccggacccc aagcccacgg ctccctcgac tctggggcac ggaaccccgc	883
ccactcccaa tccccgcgcc ccgccctctc ccacccgtgc ttcccccgct ccacccctca	943
cctcacctcg cccccgcccc acccatcgcg ccccggcggc tgttattgtt cggctgggct	1003
cggtcgggcg ctgtctccct cggctctgcg ggtgtcagtt cgtccggctt cctcacagcc	1063
cctcactccc ggcggctgac agcagcagcg gcggcgccgg gcggcgccctg gcgtttcgag	1123
gctgagcggc accgggggtt gggcgccggg gaggagcagc agcgggagga ggagccgtgt	1183
gccctggcac tgagcggccg cggccatggc gtacgcctat ctcttcaagt acatcataat	1243
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ccagtgcacg accttactat tgggtgtagag ttccggtgctc gaatgataac tattgatggg	1363
aaacagataa aacttcagat atgggatacg gcagggcaag aatcctttcg ttccatcaca	1423
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acattcaacc acttgacaac ctggttagaa gatccccgcc agcattccaa ttccaacatg	1543
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<210> 72
 <211> 252
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..17

<220>
 <221> UNSURE
 <222> 156
 <223> Xaa = Ala,Gly

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 1 5 10 15
 Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu Leu Tyr
 20 25 30

Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile Ala Ala
 35 40 45
 Thr Pro Ala Ser Ala Ala Ala Thr Leu Asp Val Ala Val Arg Arg
 50 55 60
 Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu Gly Gln
 65 70 75
 Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu Trp Leu
 80 85 90 95
 Asn Ile Arg Gly Lys Glu Ala Ala Ala Leu Ser Met Phe His Val Ser
 100 105 110
 Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile Leu Gly
 115 120 125
 Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val Leu Val
 130 135 140
 Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Xaa Ala Leu Leu
 145 150 155
 Ala Ala Met Leu Arg Gly Leu Ala Gly Gly Arg Val Leu Ala Leu Leu
 160 165 170 175
 Glu Glu Asn Ser Thr Pro Gln Leu Ala Gly Ile Leu Ala Arg Val Leu
 180 185 190
 Asn Gly Glu Ala Pro Pro Ser Leu Gly Pro Ser Ser Val Ala Ser Pro
 195 200 205
 Glu Asp Val Gln Ala Leu Met Tyr Leu Arg Gly Gln Leu Glu Pro Gln
 210 215 220
 Trp Lys Met Leu Gln Cys His Pro His Leu Val Ala
 225 230 235

<210> 73
 <211> 879
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..8

<220>
 <221> CDS
 <222> 9..395

<220>
 <221> 3'UTR
 <222> 396..879

<220>
 <221> polyA_site
 <222> 864..879

<400> 73
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 Pro Gly Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser
 1 5 10 15
 cca ggg ttc ccc gcc agg ccc ggg agg ggg cgg ccg tac atg gcc agc 146
 Pro Gly Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser
 20 25 30
 agg cct ccg ggg gac ctc gcc gag gct gga ggc cga gct ctg cag agc 194
 Arg Pro Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser
 35 40 45
 tta caa ttg aga ctg cta acc cct acc ttt gaa ggg atc aac gga ttg 242
 Leu Gln Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu

50	55	60	
ttg ttg aaa caa cat tta gtt cag aat cca gtc aga ctc tgg caa ctt	290		
Leu Leu Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu			
65	70	75	
tta ggt ggt act ttc tat ttt aac acc tca agg ttg aag cag aag aat	338		
Leu Gly Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn			
80	85	90	95
aag gag aag gat aag tcg aag ggg aag gcg cct gaa gag gac gaa ggt	386		
Lys Glu Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly			
100	105	110	
ata ttc atc tgatgttctt cagtcagtag ctgcctctgg atgtctttac	435		
Ile Phe Ile			
rtttctgttt wccttttagc aaggtgaaac cagtctggam aatggggaga tggggccgggt	495		
gcagtggctc acacttgtaa tcgaaacgct ttgggaggcc caggtggaag gatcacttga	555		
ggcctatacc acatagctag accctgtctc actgcaaatt aaaaggctgg gcgtggtggc	615		
tcacacctgt aatcccagca ctttgggagg ctgaggcagg cggatcacct gcaccctggc	675		
caacatggtg aaaccccgtc ttactaaaa atagaaaatt agccgggcgt gatggcacac	735		
gcctgtaatc ccagctactc gggaggctga ggcaggagaa ttgcttgaac ctgggagggtg	795		
gaggttgctg tgagtggaga tcatgccatt gcactccagc ctgagcaaca agagcaaaaac	855		
tccatcccaa aaaaaaaaaa aaaa	879		

<210> 74
 <211> 129
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..16

<400> 74	
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Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser Pro Gly	
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Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser Arg Pro	
20	25 30
Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser Leu Gln	
35	40 45
Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu Leu Leu	
50	55 60
Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu Leu Gly	
65	70 75 80
Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn Lys Glu	
85	90 95
Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly Ile Phe	
100	105 110
Ile	

<210> 75
 <211> 1634
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..87

<220>
 <221> CDS
 <222> 88..1269

<220>

<221> 3'UTR
 <222> 1270..1634

<220>
 <221> polyA_signal
 <222> 1594..1599

<220>
 <221> polyA_site
 <222> 1619..1634

<400> 75
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 agagtcacgc cctgtcgggg ctaggat atg atg ggt gtg ttt gta gtt gct gct 114
 Met Met Gly Val Phe Val Val Ala Ala
 1 5
 aag cga acg ccc ttt gga gct tac gga ggc ctt ctg aaa gac ttc act 162
 Lys Arg Thr Pro Phe Gly Ala Tyr Gly Gly Leu Leu Lys Asp Phe Thr
 10 15 20 25
 gct act gac ttg tct gaa ttt gct gcc aag gct gcc ttg tct gct ggc 210
 Ala Thr Asp Leu Ser Glu Phe Ala Ala Lys Ala Ala Leu Ser Ala Gly
 30 35 40
 aaa gtc tca cct gaa aca gtt gac agt gtg att atg ggc aat gtc ctg 258
 Lys Val Ser Pro Glu Thr Val Asp Ser Val Ile Met Gly Asn Val Leu
 45 50 55
 cag agt tct tca gat gct ata tat ttg gca agg cat gtt ggt ttg cgt 306
 Gln Ser Ser Ser Asp Ala Ile Tyr Leu Ala Arg His Val Gly Leu Arg
 60 65 70
 gtg gga atc cca aag gag acc cca gct ctc acg att aat agg ctc tgt 354
 Val Gly Ile Pro Lys Glu Thr Pro Ala Leu Thr Ile Asn Arg Leu Cys
 75 80 85
 ggt tct ggt ttt cag tcc att gtg aat gga tgt cag gaa att tgt gtt 402
 Gly Ser Gly Phe Gln Ser Ile Val Asn Gly Cys Gln Glu Ile Cys Val
 90 95 100 105
 aaa gaa gct gaa gtt gtt tta tgt gga gga acc gaa agc atg agc caa 450
 Lys Glu Ala Glu Val Val Leu Cys Gly Gly Thr Glu Ser Met Ser Gln
 110 115 120
 gct ccc tac tgt gtc aga aat gtg cgt ttt gga acc aag ctt gga tca 498
 Ala Pro Tyr Cys Val Arg Asn Val Arg Phe Gly Thr Lys Leu Gly Ser
 125 130 135
 gat atc aag ctg gaa gat tct tta tgg gta tca tta aca gat cag cat 546
 Asp Ile Lys Leu Glu Asp Ser Leu Trp Val Ser Leu Thr Asp Gln His
 140 145 150
 gtc cag ctc ccc atg gca atg act gca gag aat ctt gct gta aaa cac 594
 Val Gln Leu Pro Met Ala Met Thr Ala Glu Asn Leu Ala Val Lys His
 155 160 165
 aaa ata agc aga gaa gaa tgt gac aaa tat gcc ctg cag tca cag cag 642
 Lys Ile Ser Arg Glu Glu Cys Asp Lys Tyr Ala Leu Gln Ser Gln Gln
 170 175 180 185
 aga tgg aaa gct gct aat gat gct ggc tac ttt aat gat gaa atg gca 690
 Arg Trp Lys Ala Ala Asn Asp Ala Gly Tyr Phe Asn Asp Glu Met Ala
 190 195 200
 cca att gaa gtg aag aca aag aaa gga aaa cag aca atg cag gta gac 738
 Pro Ile Glu Val Lys Thr Lys Lys Gly Lys Gln Thr Met Gln Val Asp
 205 210 215
 gag cat gct cgg ccc caa acc acc ctg gaa cag tta cag aaa ctt cct 786
 Glu His Ala Arg Pro Gln Thr Thr Leu Glu Gln Leu Gln Lys Leu Pro
 220 225 230
 cca gta ttc aag aaa gat gga act gtt act gca ggg aat gca tcg ggt 834
 Pro Val Phe Lys Lys Asp Gly Thr Val Thr Ala Gly Asn Ala Ser Gly
 235 240 245
 gta gct gat ggt gct gga gct gtt atc ata gct agt gaa gat gct gtt 882
 Val Ala Asp Gly Ala Gly Ala Val Ile Ile Ala Ser Glu Asp Ala Val

250	255	260	265	
aag aaa cat aac ttc	aca cca ctg gca	aga att gtg ggc tac ttt	gta	930
Lys Lys His Asn Phe	Thr Pro Leu Ala Arg	Ile Val Gly Tyr Phe	Val	
	270	275	280	
tct gga tgt gat ccc	tct atc atg ggt	att ggt cct gtc cct	gct atc	978
Ser Gly Cys Asp Pro	Ser Ile Met Gly	Ile Gly Pro Val Pro	Ala Ile	
	285	290	295	
agt ggg gca ctg aag	aaa gca gga ctg	agt ctt aag gac atg	gat ttg	1026
Ser Gly Ala Leu Lys	Lys Ala Gly Leu	Ser Leu Lys Asp	Met Asp Leu	
	300	305	310	
gta gag gtg aat gaa	gct ttt gct ccc	cag tac ttg gct	gtt gag agg	1074
Val Glu Val Asn Glu	Ala Phe Ala Pro	Gln Tyr Leu Ala	Val Glu Arg	
	315	320	325	
agt ttg gat ctt gac	ata agt aaa acc	aat gtg aat gga	gga gcc att	1122
Ser Leu Asp Leu Asp	Ile Ser Lys Thr	Asn Val Asn Gly	Gly Ala Ile	
	330	335	340	345
gct ttg ggt cac cca	ctg gga gga tct	gga tca aga att	act gca cac	1170
Ala Leu Gly His Pro	Leu Gly Gly Ser	Gly Ser Arg Ile	Thr Ala His	
	350	355	360	
ctg gtt cac gaa tta	agg cgt cga ggt	gga aaa tat gcc	gtt gga tca	1218
Leu Val His Glu Leu	Arg Arg Arg Gly	Gly Lys Tyr Ala	Val Gly Ser	
	365	370	375	
gct tgc att gga ggt	ggc caa ggt att	gct gtc atc att	cag agc aca	1266
Ala Cys Ile Gly Gly	Gly Gln Gly Ile	Ala Val Ile Ile	Gln Ser Thr	
	380	385	390	
gcc tgaagagacc agt	gagctca ctgtgaccca	tccttactct acttggccag		1319
Ala				
gccacagtaa aacaagt	gac cttcagagca	gctgccacaa ctggccatgc	cctgccattg	1379
aaacagtgat taagttt	gat caagccatgg	tgacacaaaa atgcattgat	catgaatagg	1439
agcccatgct agaagt	acat tctctcagat	ttgaaccagt gaaatatgat	gtattttctga	1499
gctaaaactc aactat	agaa gacattaaaa	gaaatcgtat tcttgccaag	taaccaccac	1559
ttctgcctta gataat	atga ttataaggaa	atcaaataaa tgttgccctta	acttcaaaca	1619
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<210> 76

<211> 394

<212> PRT

<213> Homo sapiens

<400> 76

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	20	25	30
Ala Ala Lys Ala Ala	Leu Ser Ala Gly	Lys Val Ser Pro	Glu Thr Val
	35	40	45
Asp Ser Val Ile Met	Gly Asn Val Leu	Gln Ser Ser Ser	Asp Ala Ile
	50	55	60
Tyr Leu Ala Arg His	Val Gly Leu Arg	Val Gly Ile Pro	Lys Glu Thr
	65	70	75
Pro Ala Leu Thr Ile	Asn Arg Leu Cys	Gly Ser Gly Phe	Gln Ser Ile
	85	90	95
Val Asn Gly Cys Gln	Glu Ile Cys Val	Lys Glu Ala Glu	Val Val Leu
	100	105	110
Cys Gly Gly Thr Glu	Ser Met Ser Gln	Ala Pro Tyr Cys	Val Arg Asn
	115	120	125
Val Arg Phe Gly Thr	Lys Leu Gly Ser	Asp Ile Lys Leu	Glu Asp Ser
	130	135	140
Leu Trp Val Ser Leu	Thr Asp Gln His	Val Gln Leu Pro	Met Ala Met
	145	150	155
Thr Ala Glu Asn Leu	Ala Val Lys His	Lys Ile Ser Arg	Glu Glu Cys
	165	170	175
Asp Lys Tyr Ala Leu	Gln Ser Gln Gln	Arg Trp Lys Ala	Ala Asn Asp

<221> SIGNAL
 <222> 1..21

<400> 78
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 His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val Glu Asp
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 15 20 25
 Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu Lys Glu
 30 35 40
 Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser Asp Asp
 45 50 55
 Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met Gly Thr
 60 65 70 75
 Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val Lys Ser
 80 85 90
 Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys Lys Ser
 95 100 105
 Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile Thr Asp
 110 115 120
 Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe Phe Val
 125 130 135
 Ser Ser Ser Gln Gly Leu Ser Glu Leu His Ile Glu Asn Leu Asn Met
 140 145 150 155
 Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser Lys Gly
 160 165 170
 Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu Ala Ala
 175 180 185
 Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu Val Thr
 190 195 200
 Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val Leu Asp
 205 210 215
 Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln His Gln
 220 225 230 235
 Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser
 240 245

<210> 79
 <211> 1466
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..343

<220>
 <221> CDS
 <222> 344..1144

<220>
 <221> 3'UTR
 <222> 1145..1466

<400> 79
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 aattggcagc cttagaacta gtgggaaggc ggggtgcgcga agtcgagggg cggagagagg 120
 gggccggagg agctgctttc tgaatccaag ttcgtgggct ctctcagaag tcctcaggac 180
 ggagcagagg tggccggcgg gcccggtga ctgcgcctyt gctttctttc cataaccttt 240
 tctttcggac tcgaatcacg gctgctgcga agggctctagt tccggacact aggggtgcccc 300
 aacgcgctga tgccccgagt gctcgcaggg cttcccgccta acc atg ctg ccg ccg 355

<220>
 <221> SIGNAL
 <222> 1..30

<400> 80
 Met Leu Pro Pro Pro Arg Pro Ala Ala Ala Leu Ala Leu Pro Val Leu
 -30 -25 -20 -15
 Leu Leu Leu Leu Val Val Leu Thr Pro Pro Pro Thr Gly Ala Arg Pro
 -10 -5 1
 Ser Pro Gly Pro Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala
 5 10 15
 Glu Gly Glu Gly Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro
 20 25 30
 Arg Gly Cys Leu Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp
 35 40 45 50
 Glu Cys Ala Asn Leu Glu Gly Gln Leu Cys Asp Leu Asp Pro Ser Ala
 55 60 65
 His Phe Tyr Gly His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr
 70 75 80
 Gly Gly Asp Leu Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys
 85 90 95
 Arg Ser Gln Ser Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln
 100 105 110
 Ile Cys Arg Leu Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu
 115 120 125 130
 Thr Val Ala His Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser
 135 140 145
 His Pro Tyr Asp Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly
 150 155 160
 Cys Glu Val Phe Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp
 165 170 175
 Gly Leu Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln
 180 185 190
 Phe Arg Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile
 195 200 205 210
 Gln Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Pro
 215 220 225
 Met Pro Trp Val Lys Trp Arg Pro Leu Leu Ala
 230 235

<210> 81
 <211> 1406
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..26

<220>
 <221> CDS
 <222> 27..689

<220>
 <221> 3'UTR
 <222> 690..1406

<220>
 <221> polyA_signal
 <222> 1302..1307

<220>
 <221> polyA_site

<222> 1325..1406

<400> 81

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GlyLeuArgAlaLeuCysArgValLeuLeuPheLeuSerGlnPheCys
-20-15-10
attctgtcgggcgggtgaaagtagtgaatccactgaaatccacttatgtgatgaag149
IleLeuSerGlyGlyGluSerThrGluIleProProTyrValMetLys
-51510
tgtccgagcaaatgggttgttgtagcaggcttcctgcaagctgtgatagac197
CysProSerAsnGlyLeuCysSerArgLeuProAlaAspCysIleAsp
152025
tgcacaacaataatctctcctgtaccatatgggaagcctgtcacttttgac245
CysThrThrAsnPheSerCysThrTyrGlyLysProValThrPheAsp
303540
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CysAlaValLysProSerValThrCysValAspGlnAspPheLysSer
455055
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GlnLysAsnPheIleIleAsnMetThrCysArgPheCysTrpGlnLeu
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ProGluThrAspTyrGluCysThrAsnSerThrSerCysMetThrVal
75808590
tcctgtcctcggcagcgcctaccgccaacctgcacggtgcgggacac437
SerCysProArgGlnArgTyrProAlaAsnCysThrValArgAspHis
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ValHisCysLeuGlyAsnArgThrPheProLysMetLeuTyrCysAsn
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TrpThrGlyGlyTyrLysTrpSerThrAlaLeuAlaLeuSerIleThr
125130135
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LeuGlyGlyPheGlyAlaAspArgPheTyrLeuGlyGlnTrpArgGlu
140145150
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GlyLeuGlyLysLeuPheSerPheGlyGlyLeuGlyIleTrpThrLeu
155160165170
atagacgtcctgctcattggaagtggctgtgtggacacagagggc677
IleAspValLeuLeuIleGlyValGlyTyrValGlyProAlaAspGly
175180185
tcttgttacatttagctgtggtgtgtgcttcaaaaaggagcagggcttagaa729
SerLeuTyrIle
190
aaagcccttttgtccgtaggagttgatgtggtgtgagtgaatatatttcta789
gtacagcatctgtactttgtttgccttgataaaggtaagataaatgaaacgctgaactat849
gctaactctggaatttgtttttatgtgctgaaatatatttttctgtgaaaaattaaa909
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<210> 82

<211> 221

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..32

<400> 82
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 -15 -10 -5
 Thr Glu Ile Pro Pro Tyr Val Met Lys Cys Pro Ser Asn Gly Leu Cys
 1 5 10 15
 Ser Arg Leu Pro Ala Asp Cys Ile Asp Cys Thr Thr Asn Phe Ser Cys
 20 25 30
 Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys Ala Val Lys Pro Ser Val
 35 40 45
 Thr Cys Val Asp Gln Asp Phe Lys Ser Gln Lys Asn Phe Ile Ile Asn
 50 55 60
 Met Thr Cys Arg Phe Cys Trp Gln Leu Pro Glu Thr Asp Tyr Glu Cys
 65 70 75 80
 Thr Asn Ser Thr Ser Cys Met Thr Val Ser Cys Pro Arg Gln Arg Tyr
 85 90 95
 Pro Ala Asn Cys Thr Val Arg Asp His Val His Cys Leu Gly Asn Arg
 100 105 110
 Thr Phe Pro Lys Met Leu Tyr Cys Asn Trp Thr Gly Gly Tyr Lys Trp
 115 120 125
 Ser Thr Ala Leu Ala Leu Ser Ile Thr Leu Gly Gly Phe Gly Ala Asp
 130 135 140
 Arg Phe Tyr Leu Gly Gln Trp Arg Glu Gly Leu Gly Lys Leu Phe Ser
 145 150 155 160
 Phe Gly Gly Leu Gly Ile Trp Thr Leu Ile Asp Val Leu Leu Ile Gly
 165 170 175
 Val Gly Tyr Val Gly Pro Ala Asp Gly Ser Leu Tyr Ile
 180 185

<210> 83
 <211> 1754
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..117

<220>
 <221> CDS
 <222> 118..510

<220>
 <221> 3'UTR
 <222> 511..1754

<220>
 <221> polyA_signal
 <222> 1718..1723

<220>
 <221> polyA_site
 <222> 1739..1754

<400> 83

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 gcggttcgcc ccgcagcctc gccccctgcc caccggggcg gccgtagggc ggtcacg 117
 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg 165
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
 -20 -15 -10
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
 -5 1 5
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
 10 15 20 25
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
 30 35 40
 ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
 45 50 55
 cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
 60 65 70
 atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
 75 80 85
 cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
 90 95 100 105
 ggc ccc agc tgaccgcccc agcccgcgct gattgcacct gtctgcattc 550
 Gly Pro Ser
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 gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670
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 tagactggaa aaaagccagt cttaaaggcct ctggatactg ggctccccag aactgctggc 1690
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 aaaa 1754

<210> 84
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

<400> 84
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 -20 -15 -10
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro

Ile	Leu	Gln	Gln	Gly	Gln	Cys	Gly	Glu	Gly	His	Pro	Ala	Arg	Thr	Leu	
75					80						85					
cct	ccc	agg	ccc	ctg	ggg	cag	ccc	tcc	cgc	cgc	agg	ttt	cag	gtc	cca	501
Pro	Pro	Arg	Pro	Leu	Gly	Gln	Pro	Ser	Arg	Arg	Arg	Phe	Gln	Val	Pro	
90				95				100					105			
ggc	ccc	agc	tgacc	gcccc	agcccc	gcgct	gattg	cacct	gtctg	catte						550
Gly	Pro	Ser														
acagacattc	gggagacggc	cttcgtgttc	gccatcactg	cggccggcgc	cagccacgcc											610
gtcacgcagg	cctgttctat	gggcgagctg	ctgcagtgcg	gctgccaggc	gccccgcggg											670
cgggccccctc	cccggccctc	cggcctgccc	ggcacccccg	gacccccctg	ccccgcgggc											730
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gcgttggtgc	aactgcacaa	caacgaggcg	ggcaggctgg	ccgtgcggag	ccacacgcgc											910
accgagtgc	aatgccacgg	gctgtcggga	tcattgcgcg	tgccgacctg	ctggcagaag											970
ctgcctccat	ttcgcgaggt	gggcgcgcgg	ctgctggagc	gcttycacgg	cgcctcacgc											1030
gtcatgggca	ccaacgacgg	caaggccctg	ctgccgcgcg	tccgcacgct	caagccgcgc											1090
ggccgagcgg	acctcctcta	cgcgcgcgat	tcgcccgcg	tctgcgcgcc	caaccgacgc											1150
accggctccc	ccggcacgcg	cggtcgcgcg	tgcaatagca	gcgccccgga	cctcagcggc											1210
tgcgacctgc	tgtgctgcgg	ccgcggggcac	cgccaggaga	gcgtgcagct	cgaagagaac											1270
tgcctgtgcc	gcttccactg	gtgctgcgta	gtacagtgcc	accgctgccg	tgtgcgcaag											1330
gagctcagcc	tctgcctgtg	acccgcgcgc	cggccgctag	actgacttcg	cgcagcgggtg											1390
gctcgcacct	gtgggacctc	agggcaccgg	caccgggcgc	ctctcgccgc	tcgagcccag											1450
cctctccctg	ccaaagccca	actcccaggg	ctctggaaat	ggtgaggcga	ggggcttgag											1510
aggaacgccc	acccacgaag	gcccaggggc	ccagacggcc	ccgaaaaggc	gctcggggag											1570
cgtttaaagg	acactgtaca	ggccctccct	ccccttgcc	tctaggagga	aacagttttt											1630
tagactggaa	aaaagccagt	ctaaaggcct	ctggatactg	ggctccccag	aactgctggc											1690
cacaggatgg	tgggtgaggt	tagtatcaat	aaagatattt	aaaccaccaa	aaaaaaaaaa											1750
aaaa																1754

<210> 86
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> 1..24

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				-20					-15					-10		
Leu	Cys	Pro	Ala	His	Val	Gly	Gly	Leu	Trp	Trp	Ala	Val	Gly	Ser	Pro	
			-5					1			5					
Leu	Val	Met	Asp	Pro	Thr	Ser	Ile	Cys	Arg	Lys	Ala	Arg	Arg	Leu	Ala	
10					15						20					
Gly	Arg	Gln	Ala	Glu	Leu	Cys	Gln	Ala	Glu	Pro	Glu	Val	Val	Ala	Glu	
25				30					35					40		
Leu	Ala	Arg	Gly	Ala	Arg	Leu	Gly	Val	Arg	Glu	Cys	Gln	Phe	Gln	Phe	
			45					50					55			
Arg	Phe	Arg	Arg	Trp	Asn	Cys	Ser	Ser	His	Ser	Lys	Ala	Phe	Gly	Arg	
			60				65					70				
Ile	Leu	Gln	Gln	Gly	Gln	Cys	Gly	Glu	Gly	His	Pro	Ala	Arg	Thr	Leu	
75					80						85					
Pro	Pro	Arg	Pro	Leu	Gly	Gln	Pro	Ser	Arg	Arg	Arg	Phe	Gln	Val	Pro	
90					95						100					
Gly	Pro	Ser														
105																

<210> 87
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..151

<220>
 <221> CDS
 <222> 152..655

<220>
 <221> 3'UTR
 <222> 656..1431

<220>
 <221> polyA_signal
 <222> 1399..1404

<220>
 <221> polyA_site
 <222> 1416..1431

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 gcccaaacca aggcccccag agaggtcccc caggcccctt tgggtccctg agcctcagct 120
 ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
 Met Leu Phe Arg Leu Ser Glu
 1 5
 cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
 His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
 10 15 20
 gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268
 Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
 25 30 35
 cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
 Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
 40 45 50 55
 tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
 Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu
 60 65 70
 ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
 Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu
 75 80 85
 gaa gag gag gat gat gaa gaa gag gaa gaa gaa gag gac agc cag gct 460
 Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala
 90 95 100
 gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
 Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys
 105 110 115
 ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
 Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu
 120 125 130 135
 tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604
 Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu
 140 145 150
 agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652
 Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly
 155 160 165
 aca taggcacca gcctgcatct ccaggagga agtggagggg acatcgctgt 705
 Thr
 tccccagaaa cccactctat cctcaccctg ttttgtgctc ttcccctcgc ctgctagggc 765
 tgcggcttct gacttctaga agactaaggc tgggtctgtgt ttgcttggtt gccaccttt 825
 ggctgatacc cagagaacct gggcacttgc tgcctgatgc ccacccctgc cagtcattcc 885
 tccattcacc cagcgggagg tgggatgtga gacagccac attggaaaat ccagaaaacc 945
 ggaacaggg atttgccctt cacaattcta ctccccagat cctctcccct ggacacagga 1005

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gacccacagg gcaggaccct aagatctggg gaaaggaggt cctgagaacc ttgaggtacc 1065
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gcttctacca ggggccagga ctaaggcgtt tttctccata gcctcaacat tttgggaatc 1185
ttcccttaat cacccttgct cctcctgggt gcctggaaga tggactggca gagacctctt 1245
tgttgcgttt tgtgctttga tgccaggaat gccgcctagt ttatgtcccc ggtggggcac 1305
acagcggggg gcgccaggtt ttccttgctt cccagctgct ctgccccttt ccccttcttc 1365
cctgactcca ggccgaacc cctcccgtgc tgtaataaat ctttgtaaag aaaaaaaaaa 1425
aaaaaa                                           1431

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<210> 88
<211> 168
<212> PRT
<213> Homo sapiens

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<400> 88
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1          5          10          15
Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg
          20          25          30
Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg
          35          40          45
Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln
          50          55          60
Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr
65          70          75          80
Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu
          85          90          95
Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser
          100          105          110
Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu
          115          120          125
Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp
          130          135          140
Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
145          150          155          160
Pro Ser Pro Ser Glu Pro Gly Thr
          165

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<210> 89
<211> 1431
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..151

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<220>
<221> CDS
<222> 152..655

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<220>
<221> 3'UTR
<222> 656..1431

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<220>
<221> polyA_signal
<222> 1399..1404

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<220>
<221> polyA_site
<222> 1416..1431

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gccccaaacca agggccccag agagggtcccc caggccccctt tgggtccctg agcctcagct 120
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctg tca gag 172
Met Leu Phe Arg Leu Ser Glu
1 5
cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
10 15 20
gag ggg cac cat ctg aag tgc aag aga ccc aac ccc tgt gcc tac aca 268
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
25 30 35
cca cct tgc ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
40 45 50 55
tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu
60 65 70
ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu
75 80 85
gaa gag gag gat gat gaa gaa gag gaa gaa gaa gag gac agc cag gct 460
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala
90 95 100
gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys
105 110 115
ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu
120 125 130 135
tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604
Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu
140 145 150
agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly
155 160 165
aca taggcacca gcctgcatct cccaggagga agtggagggg acatcgctgt 705
Thr
tccccagaaa cccactctat cctcaccctg ttttgtgctc ttccccctgc ctgctagggc 765
tgcggcttct gacttctaga agactaaggc tgggtctgtgt ttgcttggtt gccaccttt 825
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tccattcacc cagcgggagg tgggatgtga gacagccac attggaaaat ccagaaaacc 945
gggaacaggg atttgccctt cacaattcta ctccccagat cctctccccct ggacacagga 1005
gacccacagg gcaggaccct aagatctggg gaaaggagggt cctgagaacc ttgaggtacc 1065
cttagatcct tttctaccca ctttctatg gaggattcca agtcaccact tctctaccg 1125
gcttctacca ggggtccagga ctaaggcggt tttctccata gcctcaacat tttgggaatc 1185
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tgttgcgttt tgtgctttga tgccaggaat gccgcctagt ttatgtcccc ggtggggcac 1305
acagcggggg gcgccagggt ttcctgtcc ccagctgct ctgccccctt ccccttcttc 1365
cctgactcca ggcctgaacc cctcccgtgc tgtaataaat ctttgtaaag aaaaaaaaaa 1425
aaaaaa 1431

<210> 90

<211> 168

<212> PRT

<213> Homo sapiens

<400> 90

Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser
1 5 10 15
Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg
20 25 30
Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg

35 40 45
 Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln
 50 55 60
 Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr
 65 70 75 80
 Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu
 85 90 95
 Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser
 100 105 110
 Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu
 115 120 125
 Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp
 130 135 140
 Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
 145 150 155 160
 Pro Ser Pro Ser Glu Pro Gly Thr
 165

<210> 91
 <211> 1417
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..47

<220>
 <221> CDS
 <222> 48..1301

<220>
 <221> 3'UTR
 <222> 1302..1417

<220>
 <221> polyA_signal
 <222> 1360..1365

<220>
 <221> polyA_site
 <222> 1402..1417

<400> 91
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 Met Pro Ser
 tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104
 Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
 -20 -15 -10 -5
 cct gtc tcc ctg gct gag gat ccc cag gga gat gct gcc cag aag aca 152
 Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr
 1 5 10
 gat aca tcc cac cat gat cag gat cac cca acc ttc aac aag atc acc 200
 Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr
 15 20 25
 ccc aac ctg gct gag ttc gcc ttc agc cta tac cgc cag ctg gca cac 248
 Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His
 30 35 40
 cag tcc aac agc acc aat atc ttc ttc tcc cca gtg agc atc gct aca 296
 Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr
 45 50 55 60
 gcc ttt gca atg ctc tcc ctg ggg acc aag gct gac act cac gat gaa 344
 Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu

				65					70				75				
atc	ctg	gag	agc	ctg	aat	ttc	aac	ctc	acg	gag	att	ccg	gag	gct	cag		392
Ile	Leu	Glu	Ser	Leu	Asn	Phe	Asn	Leu	Thr	Glu	Ile	Pro	Glu	Ala	Gln		
			80					85					90				
atc	cat	gaa	ggc	ttc	cag	gaa	ctc	ctc	cgt	acc	ctc	aac	cag	cca	gac		440
Ile	His	Glu	Gly	Phe	Gln	Glu	Leu	Leu	Arg	Thr	Leu	Asn	Gln	Pro	Asp		
		95					100					105					
agc	cag	ctc	cag	ctg	acc	acc	ggc	aat	ggc	ctg	ttc	ctc	agc	gag	ggc		488
Ser	Gln	Leu	Gln	Leu	Thr	Thr	Gly	Asn	Gly	Leu	Phe	Leu	Ser	Glu	Gly		
	110						115				120						
ctg	aag	cta	gtg	gat	aag	ttt	ttg	gag	gat	gtt	aaa	aag	ttg	tac	cac		536
Leu	Lys	Leu	Val	Asp	Lys	Phe	Leu	Glu	Asp	Val	Lys	Lys	Leu	Tyr	His		
	125				130					135					140		
tca	gaa	gcc	ttc	act	gtc	aac	ttc	ggg	gac	acc	gaa	gag	gcc	aag	aaa		584
Ser	Glu	Ala	Phe	Thr	Val	Asn	Phe	Gly	Asp	Thr	Glu	Glu	Ala	Lys	Lys		
				145					150					155			
cag	atc	aac	gat	tac	gtg	gag	aag	ggg	act	caa	ggg	aaa	att	gtg	gat		632
Gln	Ile	Asn	Asp	Tyr	Val	Glu	Lys	Gly	Thr	Gln	Gly	Lys	Ile	Val	Asp		
			160					165					170				
ttg	gtc	aag	gag	ctt	gac	aga	gac	aca	gtt	ttt	gct	ctg	gtg	aat	tac		680
Leu	Val	Lys	Glu	Leu	Asp	Arg	Asp	Thr	Val	Phe	Ala	Leu	Val	Asn	Tyr		
		175					180						185				
atc	ttc	ttt	aaa	ggc	aaa	tgg	gag	aga	ccc	ttt	gaa	gtc	aag	gac	acc		728
Ile	Phe	Phe	Lys	Gly	Lys	Trp	Glu	Arg	Pro	Phe	Glu	Val	Lys	Asp	Thr		
	190					195					200						
gag	gaa	gag	gac	ttc	cac	gtg	gac	cag	gcg	acc	acc	gtg	aag	gtg	cct		776
Glu	Glu	Glu	Asp	Phe	His	Val	Asp	Gln	Ala	Thr	Thr	Val	Lys	Val	Pro		
	205				210					215					220		
atg	atg	aag	cgt	tta	ggc	atg	ttt	aac	atc	cag	cac	tgt	aag	aag	ctg		824
Met	Met	Lys	Arg	Leu	Gly	Met	Phe	Asn	Ile	Gln	His	Cys	Lys	Lys	Leu		
				225					230					235			
tcc	agc	tgg	gtg	ctg	ctg	atg	aaa	tac	ctg	ggc	aat	gcc	acc	gcc	atc		872
Ser	Ser	Trp	Val	Leu	Leu	Met	Lys	Tyr	Leu	Gly	Asn	Ala	Thr	Ala	Ile		
			240					245					250				
ttc	ttc	ctg	cct	gat	gag	ggg	aaa	cta	cag	cac	ctg	gaa	aat	gaa	ctc		920
Phe	Phe	Leu	Pro	Asp	Glu	Gly	Lys	Leu	Gln	His	Leu	Glu	Asn	Glu	Leu		
		255					260					265					
acc	cac	gat	atc	atc	acc	aag	ttc	ctg	gaa	aat	gaa	gac	aga	agg	tct		968
Thr	His	Asp	Ile	Ile	Thr	Lys	Phe	Leu	Glu	Asn	Glu	Asp	Arg	Arg	Ser		
	270					275						280					
gcc	agc	tta	cat	tta	ccc	aaa	ctg	tcc	att	act	gga	acc	tat	gat	ctg		1016
Ala	Ser	Leu	His	Leu	Pro	Lys	Leu	Ser	Ile	Thr	Gly	Thr	Tyr	Asp	Leu		
	285				290					295					300		
aag	agc	gtc	ctg	ggg	caa	ctg	ggc	atc	act	aag	gtc	ttc	agc	aat	ggg		1064
Lys	Ser	Val	Leu	Gly	Gln	Leu	Gly	Ile	Thr	Lys	Val	Phe	Ser	Asn	Gly		
				305					310					315			
gct	gac	ctc	tcc	ggg	gtc	aca	gag	gag	gca	ccc	ctg	aag	ctc	tcc	aag		1112
Ala	Asp	Leu	Ser	Gly	Val	Thr	Glu	Glu	Ala	Pro	Leu	Lys	Leu	Ser	Lys		
			320					325					330				
gcc	gtg	cat	aag	gct	gtg	ctg	acc	atc	gac	gag	aaa	ggg	act	gaa	gct		1160
Ala	Val	His	Lys	Ala	Val	Leu	Thr	Ile	Asp	Glu	Lys	Gly	Thr	Glu	Ala		
	335						340					345					
gct	ggg	gcc	atg	ttt	tta	gag	gcc	ata	ccc	atg	tct	atc	ccc	ccc	gag		1208
Ala	Gly	Ala	Met	Phe	Leu	Glu	Ala	Ile	Pro	Met	Ser	Ile	Pro	Pro	Glu		
	350				355						360						
gtc	aag	ttc	aac	aaa	ccc	ttt	gtc	ttc	tta	atg	att	gaa	caa	aat	acc		1256
Val	Lys	Phe	Asn	Lys	Pro	Phe	Val	Phe	Leu	Met	Ile	Glu	Gln	Asn	Thr		
	365				370					375				380			
aag	tct	ccc	ctc	ttc	atg	gga	aaa	gtg	gtg	aat	ccc	acc	caa	aaa			1301
Lys	Ser	Pro	Leu	Phe	Met	Gly	Lys	Val	Val	Asn	Pro	Thr	Gln	Lys			
				385					390					395			
taactgcctc	tcgctcctca	acccctcccc	tccatccctg	gccccctccc	tggtatgacat												1361
ttaaagaaggg	ttgagctggt	ccctgcctgc	atgtgactgc	aaaaaaaaaa	aaaaaa												1417

<210> 92
 <211> 418
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

<400> 92
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 Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
 -5 1 5
 Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
 10 15 20
 Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
 25 30 35 40
 Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
 45 50 55
 Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
 60 65 70
 His Asp Glu Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro
 75 80 85
 Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
 90 95 100
 Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
 105 110 115 120
 Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
 125 130 135
 Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
 140 145 150
 Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
 155 160 165
 Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
 170 175 180
 Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
 185 190 195 200
 Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Ala Thr Thr Val
 205 210 215
 Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
 220 225 230
 Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
 235 240 245
 Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
 250 255 260
 Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
 265 270 275 280
 Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
 285 290 295
 Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
 300 305 310
 Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
 315 320 325
 Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
 330 335 340
 Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
 345 350 355 360
 Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
 365 370 375
 Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
 380 385 390

Gln Lys

<210> 93
 <211> 1115
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..277

<220>
 <221> CDS
 <222> 278..733

<220>
 <221> 3'UTR
 <222> 734..1115

<220>
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 <222> 1072..1077

<220>
 <221> polyA_site
 <222> 1101..1115

<400> 93
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 tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180
 ggaaaaacaa aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240
 gattttactt agatgattta cacaatgaag aaagtac atg cac ttt ggg ctt ctg 295
 Met His Phe Gly Leu Leu
 -15
 tcc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat tct gag 343
 Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu
 -10 -5 1
 gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca cca ctg 391
 Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu
 5 10 15 20
 aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat agc cca tgt 439
 Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Ser Pro Cys
 25 30 35
 aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga cag tgc 487
 Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys
 40 45 50
 gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga ttt gaa 535
 Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu
 55 60 65
 agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca aac agg 583
 Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg
 70 75 80
 att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc ttt ttg 631
 Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu
 85 90 95 100
 gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat 679
 Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr
 105 110 115
 aac aat cag aca aaa cat gtg aac gtt tca agt atg gtg gat gcc tgg 727
 Asn Asn Gln Thr Lys His Val Asn Val Ser Ser Met Val Asp Ala Trp
 120 125 130
 gca ata tgaacaat ttagacactg gaagaatgca agaacatttg tgaagatggg 783

Ala Ile
 ccgaatgggt tccaggtgga taattatgga acccagctca atgctgtgaa taactccctg 843
 actccgcaat caaccaaggt tcccagcctt tttgttacaa aagaaggaac aaatgatggt 903
 tggaagaatg cggctcatat ttaccaagtc tttctgaacg ctttctgcat tcatgcatcc 963
 atgttctttc taggattgga tagcatttca tgcctatggt aatatttgtg cttttggcat 1023
 ttccttaata tttatatgta tacgtgatgc ctttgatagc atactgctaa taaagtttta 1083
 atattttacat gcataggaaa aaaaaaaaaa aa 1115

<210> 94
 <211> 152
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..19

<400> 94
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 -15 -10 -5
 Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp
 1 5 10
 Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys
 15 20 25
 Ala Asp Asp Ser Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn
 30 35 40 45
 Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly
 50 55 60
 Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr
 65 70 75
 Arg Asp Asn Ala Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys
 80 85 90
 Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr
 95 100 105
 Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys His Val Asn Val Ser
 110 115 120 125
 Ser Met Val Asp Ala Trp Ala Ile
 130

<210> 95
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..252

<220>
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 <222> 253..744

<220>
 <221> 3'UTR
 <222> 745..1307

<220>
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 <222> 1269..1274

<220>
 <221> polyA_site
 <222> 1292..1307

<400> 95
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tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180
ggaaaaacag aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240
gattttactt ag atg att tac aca atg aag aaa gta cat gca ctt tgg gct 291
Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala
-25 -20 -15
tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat 339
Ser Val Cys Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp
-10 -5 1
tct gag gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca 387
Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro
5 10 15
cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat ggc 435
Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly
20 25 30
cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga 483
Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg
35 40 45 50
cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga 531
Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg
55 60 65
ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca 579
Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala
70 75 80
aac agg att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc 627
Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys
85 90 95
ttt ttg gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat 675
Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
100 105 110
ttt tat aac aat cag aca aaa cag tgt gaa cgt ttc aag tat ggt gga 723
Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
115 120 125 130
tgc ctg ggc aat caa caa ttt tgagacactg gaacaatgca agaacatttg 774
Cys Leu Gly Asn Gln Gln Phe
135
tgaagatggg ccgaatgggt tccaggtgga taattatgga acccagctca atgctgtgaa 834
taactccctg actccgcaat caaccaagggt tcccagcctt tttgaatttc acgggtccctc 894
atgggtgtctc actccagcag acagaggatt gtgtcgtgcc aatgagaaca gattctacta 954
caattcagtc attgggaaat gccgccatt taagtacagt ggatgtgggg gaaatgaaaa 1014
caattttact tccaacaag aatgtctgag ggcattgtaaa aaaggtttca tccaaagaat 1074
atcaaaagga ggcctaatta aaaccaaag aaaaagaaaag aagcagagag tgaaaatagc 1134
atatgaagaa atttttgtta aaaatatgtg aattttgttat agcaatgtaa cattaattct 1194
actaaatatt ttatatgaaa tgtttcaacta tgattttcta tttttcttct aaaatgcttt 1254
taattaatat gttcattaaa ttttctatgc ttattgcaaa aaaaaaaaaa aaa 1307

<210> 96
<211> 164
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..28

<400> 96
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-10 -5 1

Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
 5 10 15 20
 Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys
 25 30 35
 Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
 40 45 50
 Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
 55 60 65
 Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg Ile
 70 75 80
 Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu Glu
 85 90 95 100
 Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn
 105 110 115
 Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly
 120 125 130
 Asn Gln Gln Phe
 135

<210> 97
 <211> 1855
 <212> DNA
 <213> Homo sapiens

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 <222> 1..117

<220>
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 <222> 118..504

<220>
 <221> 3'UTR
 <222> 505..1855

<220>
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 <222> 1819..1824

<220>
 <221> polyA_site
 <222> 1840..1855

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 gcggttcgcc ccgcagcctc gcccctgcc caccgggcg gccgtagggc ggtcacg 117
 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctc 165
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
 -20 -15 -10
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
 -5 1 5
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
 10 15 20 25
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
 30 35 40
 ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
 45 50 55
 cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405

Arg	Phe	Arg	Arg	Trp	Asn	Cys	Ser	Ser	His	Ser	Lys	Ala	Phe	Gly	Arg		
		60					65					70					
atc	ctg	caa	cag	ggt	cag	tgt	ggg	gag	ggg	gcg	gaa	gtg	ggg	ctg	ctt	453	
Ile	Leu	Gln	Gln	Gly	Gln	Cys	Gly	Glu	Gly	Ala	Glu	Val	Gly	Leu	Leu		
		75					80					85					
tct	ccc	tgc	tgt	ggg	acc	cga	gga	gag	gag	aac	tgg	ttc	gct	gaa	gtt	501	
Ser	Pro	Cys	Cys	Gly	Thr	Arg	Gly	Glu	Glu	Asn	Trp	Phe	Ala	Glu	Val		
					95					100					105		
90																	
gcc	tgagccccac	ttccccctca	catgtgtctg	ggcaccctgc	aaggaccctg											554	
Ala																	
cctcccaggc	ccctggggca	gccctcccgc	cgcaggtttc	aggtcccagg	ccccagctga	614											
ccgccccagc	ccgcgctgat	tgacactgtc	tgcatcaca	gacattcggg	agacggcctt	674											
cgtgttcgcc	atcactgcgg	ccggcgccag	ccacgcgcgc	acgcaggcct	gttctatggg	734											
cgagctgctg	cagtgcggct	gccaggcgcc	ccgcgggcgg	gccccctccc	ggccctccgg	794											
cctgccccgc	acccccggac	cccctggccc	cgcgggctcc	ccggaaggca	gcgcgcgctg	854											
ggagtgggga	ggctgcggcg	acgacgtgga	cttcggggac	gagaagtcga	ggctctttat	914											
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cgaggcgggc	aggctggccg	tgcgagagcca	cacgcgcacc	gagtgcacaa	gccacgggct	1034											
gtcgggatca	tgcgcgctgc	gcacctgctg	gcagaagctg	cctccatttc	gcgaggtggg	1094											
cgcgcggctg	ctggagcgct	tccacggcgc	ctcacgcgtc	atgggcacca	acgacggcaa	1154											
ggccctgctg	cccgccttcc	gcacgtctca	gccgcggggc	cgagcggacc	tcctctacgc	1214											
cgcgatttcg	cccgaattct	gcgcccccaa	ccgacgcacc	ggctcccccg	gcacgcgcgg	1274											
tcgcgcctgc	aatagcagcg	ccccggacct	cagcggtctg	gacctgctgt	gctgcggccg	1334											
cgggcaccgc	caggagagcg	tgacgctcga	agagaactgc	ctgtgccgct	tcactgggtg	1394											
ctgcgtagta	cagtgccacc	gctgccgtgt	gcgcaaggag	ctcagcctct	gcctgtgacc	1454											
cgcgcgccgg	ccgctagact	gacttcgcgc	agcgtgtggc	cgcacctgtg	ggacctcagg	1514											
gcaccggcac	cgggcgcctc	tcgcgcgtcg	agcccagcct	ctccctgccca	aagcccaact	1574											
cccaggggctc	tggaatggg	gaggcgaggg	gcttgagagg	aacgcccacc	cacgaaggcc	1634											
caggggcgcca	gacggccccg	aaaaggcgct	cggggagcgt	ttaaaggaca	ctgtacaggc	1694											
cctccctccc	cttgccctct	aggaggaaac	agtttttttag	actggaaaaa	agccagtcta	1754											
aaggcctctg	gatactgggc	tccccagaac	tgctggccac	aggatggtgg	gtgaggttag	1814											
tatcaataaa	gatattttaa	ccaccaaaaa	aaaaaaaaaa	a		1855											

<210> 98
 <211> 129
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

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				-20					-15					-10			
Leu	Cys	Pro	Ala	His	Val	Gly	Gly	Leu	Trp	Trp	Ala	Val	Gly	Ser	Pro		
			-5					1				5					
Leu	Val	Met	Asp	Pro	Thr	Ser	Ile	Cys	Arg	Lys	Ala	Arg	Arg	Leu	Ala		
		10				15					20						
Gly	Arg	Gln	Ala	Glu	Leu	Cys	Gln	Ala	Glu	Pro	Glu	Val	Val	Ala	Glu		
		25			30					35				40			
Leu	Ala	Arg	Gly	Ala	Arg	Leu	Gly	Val	Arg	Glu	Cys	Gln	Phe	Gln	Phe		
			45					50						55			
Arg	Phe	Arg	Arg	Trp	Asn	Cys	Ser	Ser	His	Ser	Lys	Ala	Phe	Gly	Arg		
			60					65					70				
Ile	Leu	Gln	Gln	Gly	Gln	Cys	Gly	Glu	Gly	Ala	Glu	Val	Gly	Leu	Leu		
		75					80					85					
Ser	Pro	Cys	Cys	Gly	Thr	Arg	Gly	Glu	Glu	Asn	Trp	Phe	Ala	Glu	Val		
		90				95					100						
Ala																	
105																	

<210> 99

<211> 667
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..94

<220>
 <221> CDS
 <222> 95..613

<220>
 <221> 3'UTR
 <222> 614..667

<220>
 <221> polyA_signal
 <222> 636..641

<220>
 <221> polyA_site
 <222> 652..667

<400> 99
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 gttccatctc aacagcccct gttttggaaa ggac atg att gtc aag ggg gtg gcc 115
 Met Ile Val Lys Gly Val Ala
 1 5
 tcc aga act gtg gtt tcc aga ccg ttc ccc ggt aac tgg ctt ttc tct 163
 Ser Arg Thr Val Val Ser Arg Pro Phe Pro Gly Asn Trp Leu Phe Ser
 10 15 20
 tcc atc cag ctg act gat gat cag ggc ccc gtc ctg atg acc act gta 211
 Ser Ile Gln Leu Thr Asp Asp Gln Gly Pro Val Leu Met Thr Thr Val
 25 30 35
 gcc atg cct gtg ttt agt aag cag aac gaa acc aga tcg aag ggc att 259
 Ala Met Pro Val Phe Ser Lys Gln Asn Glu Thr Arg Ser Lys Gly Ile
 40 45 50 55
 ctt ctg gga gtg gtt ggc aca gat gtc cca gtg aaa gaa ctt ctg aag 307
 Leu Leu Gly Val Val Gly Thr Asp Val Pro Val Lys Glu Leu Leu Lys
 60 65 70
 acc atc ccc aaa tac aag tta ggg att cac ggt tat gcc ttt gca atc 355
 Thr Ile Pro Lys Tyr Lys Leu Gly Ile His Gly Tyr Ala Phe Ala Ile
 75 80 85
 aca aat aat gga tat atc ctg acg cat ccg gaa ctc agg ctg ctg tac 403
 Thr Asn Asn Gly Tyr Ile Leu Thr His Pro Glu Leu Arg Leu Leu Tyr
 90 95 100
 gaa gaa gga aaa aag cga agg aaa cct aac tat agt agc gtt gac ctc 451
 Glu Glu Gly Lys Lys Arg Arg Lys Pro Asn Tyr Ser Ser Val Asp Leu
 105 110 115
 tct gag gtg gag tgg gaa gac cga gat gac gtg ttg aga aat gct atg 499
 Ser Glu Val Glu Trp Glu Asp Arg Asp Asp Val Leu Arg Asn Ala Met
 120 125 130 135
 gtg aat cga aag acg ggg aag ttt tcc atg gag gtg aag aag aca gtg 547
 Val Asn Arg Lys Thr Gly Lys Phe Ser Met Glu Val Lys Lys Thr Val
 140 145 150
 gac aaa ggg gta cat ttt tct caa aca ttt ttg ctg ctt aat tta aaa 595
 Asp Lys Gly Val His Phe Ser Gln Thr Phe Leu Leu Leu Asn Leu Lys
 155 160 165
 caa acc act gtg aaa aat tagctttgaa agctatatct ggaataaata 643
 Gln Thr Thr Val Lys Asn
 170
 tctttcgcaa aaaaaaaaaa aaaa 667

<210> 100
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 100
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 Pro Gly Asn Trp Leu Phe Ser Ser Ile Gln Leu Thr Asp Asp Gln Gly
 20 25 30
 Pro Val Leu Met Thr Thr Val Ala Met Pro Val Phe Ser Lys Gln Asn
 35 40 45
 Glu Thr Arg Ser Lys Gly Ile Leu Leu Gly Val Val Gly Thr Asp Val
 50 55 60
 Pro Val Lys Glu Leu Leu Lys Thr Ile Pro Lys Tyr Lys Leu Gly Ile
 65 70 75 80
 His Gly Tyr Ala Phe Ala Ile Thr Asn Asn Gly Tyr Ile Leu Thr His
 85 90 95
 Pro Glu Leu Arg Leu Leu Tyr Glu Glu Gly Lys Lys Arg Arg Lys Pro
 100 105 110
 Asn Tyr Ser Ser Val Asp Leu Ser Glu Val Glu Trp Glu Asp Arg Asp
 115 120 125
 Asp Val Leu Arg Asn Ala Met Val Asn Arg Lys Thr Gly Lys Phe Ser
 130 135 140
 Met Glu Val Lys Lys Thr Val Asp Lys Gly Val His Phe Ser Gln Thr
 145 150 155 160
 Phe Leu Leu Leu Asn Leu Lys Gln Thr Thr Val Lys Asn
 165 170

<210> 101
 <211> 1062
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..153

<220>
 <221> CDS
 <222> 154..639

<220>
 <221> 3'UTR
 <222> 640..1062

<220>
 <221> polyA_signal
 <222> 1023..1028

<220>
 <221> polyA_site
 <222> 1047..1062

<400> 101
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 gagccacacg ctgggggtgc tggctgaggg aac atg gct tgt tgg cct cag ctg 174
 Met Ala Cys Trp Pro Gln Leu
 1 5
 agg ttg ctg ctg tgg aag aac ctc act ttc aga aga aga caa aca tgt 222
 Arg Leu Leu Leu Trp Lys Asn Leu Thr Phe Arg Arg Arg Gln Thr Cys

10	15	20	
cag ctg ctg ctg gaa gtg gcc tgg cct cta ttt atc ttc ctg atc ctg			270
Gln Leu Leu Leu Glu Val Ala Trp Pro Leu Phe Ile Phe Leu Ile Leu			
25	30	35	
atc tct gtt cgg ctg agc tac cca ccc tat gaa caa cat gaa tgc cat			318
Ile Ser Val Arg Leu Ser Tyr Pro Pro Tyr Glu Gln His Glu Cys His			
40	45	50	55
ttt cca aat aaa gcc atg ccc tct gca gga aca ctt cct tgg gtt cag			366
Phe Pro Asn Lys Ala Met Pro Ser Ala Gly Thr Leu Pro Trp Val Gln			
60	65	70	
ggg att atc tgt aat gcc aac aac ccc tgt ttc cgt tac ccg act cct			414
Gly Ile Ile Cys Asn Ala Asn Asn Pro Cys Phe Arg Tyr Pro Thr Pro			
75	80	85	
ggg gag gct ccc gga gtt gtt gga aac ttt aac aaa tcc att gtg gct			462
Gly Glu Ala Pro Gly Val Val Gly Asn Phe Asn Lys Ser Ile Val Ala			
90	95	100	
cgc ctg ttc tca gat gct cgg agg ctt ctt tta tac agc cag aaa gac			510
Arg Leu Phe Ser Asp Ala Arg Arg Leu Leu Leu Tyr Ser Gln Lys Asp			
105	110	115	
acc agc atg aag gac atg cgc aaa gtt ctg aga aca tta cag cag atc			558
Thr Ser Met Lys Asp Met Arg Lys Val Leu Arg Thr Leu Gln Gln Ile			
120	125	130	135
aag aaa tcc agc tca aga ggg gac aaa cgc cat ttc ctc aac tgg cag			606
Lys Lys Ser Ser Ser Arg Gly Asp Lys Arg His Phe Leu Asn Trp Gln			
140	145	150	
aag gga ctg aag cct ctc cct caa gcc ctt tta taggggtcct cattgtcagg			659
Lys Gly Leu Lys Pro Leu Pro Gln Ala Leu Leu			
155	160		
cctctaagcc caagccaagc catcgcatcc cctgtgactt gcacatatatac gcccagatgg			719
cctgaagtaa ctgaagaatc acaaaaagaag tgaaaaaggcc ctgcctcgcc ttaactgatg			779
acgttccacc attgtgattt gttcctgccc caccttaact gagtgattaa ccctgtgaat			839
ttccttctcc tggctcagaa gctccccac tgagcacctt gtgacccctt gcccctgccc			899
accagagaac aacccccctt gactgtaatt ttccattacc ttcccaaatac ctataaaacg			959
gccccacccc tatctccctt tgctgactct cttttcggac tcagcccacc tgcagccagg			1019
tgaaaaaaac agctttattg ctcacacaaa aaaaaaaaaa aaa			1062

<210> 102

<211> 162

<212> PRT

<213> Homo sapiens

<400> 102

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20	25
Leu Phe Ile Phe Leu Ile Leu Ile Ser Val Arg Leu Ser Tyr Pro Pro	
35	40
Tyr Glu Gln His Glu Cys His Phe Pro Asn Lys Ala Met Pro Ser Ala	
50	55
Gly Thr Leu Pro Trp Val Gln Gly Ile Ile Cys Asn Ala Asn Asn Pro	
65	70
Cys Phe Arg Tyr Pro Thr Pro Gly Glu Ala Pro Gly Val Val Gly Asn	
85	90
Phe Asn Lys Ser Ile Val Ala Arg Leu Phe Ser Asp Ala Arg Arg Leu	
100	105
Leu Leu Tyr Ser Gln Lys Asp Thr Ser Met Lys Asp Met Arg Lys Val	
115	120
Leu Arg Thr Leu Gln Gln Ile Lys Lys Ser Ser Ser Arg Gly Asp Lys	
130	135
Arg His Phe Leu Asn Trp Gln Lys Gly Leu Lys Pro Leu Pro Gln Ala	
145	150
Leu Leu	155
	160

<210> 103
 <211> 933
 <212> DNA
 <213> Homo sapiens

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 <222> 1..149

<220>
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 <222> 150..392

<220>
 <221> 3'UTR
 <222> 393..933

<220>
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 <222> 63..933

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 cagatgtgta cggatgaaaa tacagtggag atg agt cag aaa ccg gcc aag gag 173
 Met Ser Gln Lys Pro Ala Lys Glu
 1 5
 ggt ccc aga ctc tcc aaa aac cag aag tac tcc gaa cac ttc agc ata 221
 Gly Pro Arg Leu Ser Lys Asn Gln Lys Tyr Ser Glu His Phe Ser Ile
 10 15 20
 cac tgc tgc ccg ccg ttc acc ttc ctc aat tcc aag aag gag ata gtg 269
 His Cys Cys Pro Pro Phe Thr Phe Leu Asn Ser Lys Lys Glu Ile Val
 25 30 35 40
 gat cgg aaa tac agc atc tgt aag agc ggc tgc ttc tac cag aag aaa 317
 Asp Arg Lys Tyr Ser Ile Cys Lys Ser Gly Cys Phe Tyr Gln Lys Lys
 45 50 55
 gag gag gac tgg atc tgc tgc gcc tgc cag aag acc aga ttg aaa agg 365
 Glu Glu Asp Trp Ile Cys Cys Ala Cys Gln Lys Thr Arg Leu Lys Arg
 60 65 70
 aag atc agg cca acc cca aag aag aag tgaccaagga ggagtttaaa 412
 Lys Ile Arg Pro Thr Pro Lys Lys Lys
 75 80
 ytgaatgaac aacctcggct cctggactca ttgcttcaca acccatctac ccctggatga 472
 agttatctgg cttcaaatat tatgcagggg caaacacctg ctgatgtggc aactgctgat 532
 gctcatggtc cccatggcat gggggcctca gggcagcctg cctggagtac tttgaagatg 592
 tcatcccatt gtcttctgac ctctataatt gccactgaga gatctgctgt cagtctgctt 652
 atccttccac ggactcaagt ttcttcaatc tgaagataca tgtctttctc caaggacatg 712
 tggaaaaaaaa aaagatgtta tacaaccatc aaagtggcaa aaataaaaaa aattggctgg 772
 gcgtgggtggc gggcgctgt ggtcccagct actcgggagg ctgagggcagg agaatggcgt 832
 gaacctggga ggcggagctt gcagtgagcc gagatcgcac cactgcactc cagcctgggc 892
 gacagagcga gactctgtct caaacaaaaa aaaaaaaaaa a 933

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 <211> 81
 <212> PRT
 <213> Homo sapiens

<400> 104
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 1 5 10 15
 Lys Tyr Ser Glu His Phe Ser Ile His Cys Cys Pro Pro Phe Thr Phe
 20 25 30

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aca ctt cgt gtt tat aag cca tca gct gga aac aat tcc ctc tat cgg			535
Thr Leu Arg Val Tyr Lys Pro Ser Ala Gly Asn Asn Ser Leu Tyr Arg			
135	140	145	
gac aca gca gtt ttt gaa tgt ttg cca caa cat gcg atg ttt gga aat			583
Asp Thr Ala Val Phe Glu Cys Leu Pro Gln His Ala Met Phe Gly Asn			
150	155	160	165
gat aca att acc tgc acg aca cat gga aat tgg act aaa tta cca gaa			631
Asp Thr Ile Thr Cys Thr Thr His Gly Asn Trp Thr Lys Leu Pro Glu			
170	175	180	
tgc agg gaa gta aaa tgc cca ttc cca tca aga cca gac aat gga ttt			679
Cys Arg Glu Val Lys Cys Pro Phe Pro Ser Arg Pro Asp Asn Gly Phe			
185	190	195	
gtg aac tat cct gca aaa cca aca ctt tat tac aag gat aaa gcc aca			727
Val Asn Tyr Pro Ala Lys Pro Thr Leu Tyr Tyr Lys Asp Lys Ala Thr			
200	205	210	
ttt ggc tgc cat gat gga tat tct ctg gat ggc ccg gaa gaa ata gaa			775
Phe Gly Cys His Asp Gly Tyr Ser Leu Asp Gly Pro Glu Glu Ile Glu			
215	220	225	
tgt acc aaa ctg gga aac tgg tct gcc atg cca agt tgt aaa gca tct			823
Cys Thr Lys Leu Gly Asn Trp Ser Ala Met Pro Ser Cys Lys Ala Ser			
230	235	240	245
tgt aaa gta cct gtg aaa gcc act gtg gtg tac caa gga gag aga			871
Cys Lys Val Pro Val Lys Lys Ala Thr Val Val Tyr Gln Gly Glu Arg			
250	255	260	
gta aag att cag gaa aaa ttt aag aat gga atg cta cat ggt gat aaa			919
Val Lys Ile Gln Glu Lys Phe Lys Asn Gly Met Leu His Gly Asp Lys			
265	270	275	
gtt tct ttc ttc tgc aaa aat aag gaa aag aag tgt agc tat aca gag			967
Val Ser Phe Phe Cys Lys Asn Lys Glu Lys Lys Cys Ser Tyr Thr Glu			
280	285	290	
gat gct cag tgt ata gat ggc act atc gaa gtc ccc aaa tgc ttc aag			1015
Asp Ala Gln Cys Ile Asp Gly Thr Ile Glu Val Pro Lys Cys Phe Lys			
295	300	305	
gaa cac agt tct ctg gct ttt tgg aaa act gat gca tcc gat gta aag			1063
Glu His Ser Ser Leu Ala Phe Trp Lys Thr Asp Ala Ser Asp Val Lys			
310	315	320	325
cca tgc taagggtggtt ttcagattcc acataaaatg tcacacttgt ttcttggtca			1119
Pro Cys			
tccaaggaac ctaattgaaa tttaaaaata aagctactga atttattgcc gcaaaaaaaaa			1179
aaaaaaaa			1187

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 <212> PRT
 <213> Homo sapiens

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 <222> 1..19

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 Thr Val Val Pro Leu Lys Thr Phe Tyr Glu Pro Gly Glu Glu Ile Thr
 Tyr Ser Cys Lys Pro Gly Tyr Val Ser Arg Gly Gly Met Arg Lys Phe
 Ile Cys Pro Leu Thr Gly Leu Trp Leu Ile Asn Thr Leu Lys Cys Thr
 Pro Arg Val Cys Pro Phe Ala Gly Ile Leu Glu Asn Gly Ala Val Arg

agc tcg aaa agc gat gcc gat tct ggt ttc ctg ggg ctg cgg ccc act	99
Ser Ser Lys Ser Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr	
15 20 25	
tcg gtg gac cca gcg ctg agg cgg cgg cgg cga ggc cca aga aat aag	147
Ser Val Asp Pro Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys	
30 35 40	
aag cgg ggc tgg cgg cgg ctt gct cag gag ccg ctg ggg ctg gag gtt	195
Lys Arg Gly Trp Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val	
45 50 55 60	
gac cag ttc ctg gaa gac gtg cgg cta cag gag cgc acg agc ggt ggc	243
Asp Gln Phe Leu Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly	
65 70 75	
ttg ttg tca gag gcc cca aat gaa aaa ctc ttc ttc gtg gac act ggc	291
Leu Leu Ser Glu Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly	
80 85 90	
tcc aag gaa aaa ggg ctg aca aag aag aga acc aaa gtc cag aag aag	339
Ser Lys Glu Lys Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys	
95 100 105	
tca ctg ctt ctc aag aaa ccc ctt cgg gtt gac ctc atc ctc gag aac	387
Ser Leu Leu Leu Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn	
110 115 120	
aca tcc aaa gtc cct gcc ccc aaa gac gtc ctc gcc cac cag gtc ccc	435
Thr Ser Lys Val Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro	
125 130 135 140	
aac gcc aag aag ctc agg cgg aag gag cag cta tgg gag aag ctg gcc	483
Asn Ala Lys Lys Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala	
145 150 155	
aag cag ggc gag ctg ccc cgg gag gtg cgc agg gcc cag gcc cgg ctc	531
Lys Gln Gly Glu Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu	
160 165 170	
ctc aac cct tct gca aca agg gcc aag ccc ggg ccc cag gac acc gta	579
Leu Asn Pro Ser Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val	
175 180 185	
gag cgg ccc ttc tac gac ctc tgg gcc tca gac aac ccc ctg gac agg	627
Glu Arg Pro Phe Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg	
190 195 200	
ccg ttg gtt ggc cag gat gag ttt ttc ctg gag cag acc aag aag aaa	675
Pro Leu Val Gly Gln Asp Glu Phe Phe Leu Glu Gln Thr Lys Lys Lys	
205 210 215 220	
gga gtg aag cgg cca gca cgc ctg cac acc aag ccg tcc cag gca ccc	723
Gly Val Lys Arg Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro	
225 230 235	
gcc gtg gag gtg gcg cct gcc gga gct tcc tac aat cca tcc ttt gaa	771
Ala Val Glu Val Ala Pro Ala Gly Ala Ser Tyr Asn Pro Ser Phe Glu	
240 245 250	
gac cac cag acc ctg ctc tca gcg gcc cac gag gtg gag ttg cag cgg	819
Asp His Gln Thr Leu Leu Ser Ala Ala His Glu Val Glu Leu Gln Arg	
255 260 265	
cag aag gag gcg gag aag ctg gag cgg cag ctg gcc ctg ccc gcc acg	867
Gln Lys Glu Ala Glu Lys Leu Glu Arg Gln Leu Ala Leu Pro Ala Thr	
270 275 280	
gag cag gcc gcc acc cag gag tcc aca ttc cag gag ctg tgc gag ggg	915
Glu Gln Ala Ala Thr Gln Glu Ser Thr Phe Gln Glu Leu Cys Glu Gly	
285 290 295 300	
ctg ctg gag gag tcg gat ggt gag ggg gag cca ggc cag ggc gag ggg	963
Leu Leu Glu Glu Ser Asp Gly Glu Gly Glu Pro Gly Gln Gly Glu Gly	
305 310 315	
ccg gag gct ggg gat gcc gag gtc tgt ccc acg ccc gcc cgc ctg gcc	1011
Pro Glu Ala Gly Asp Ala Glu Val Cys Pro Thr Pro Ala Arg Leu Ala	
320 325 330	
acc aca gag aag aag acg gag cag cag cgg cgg cgg gag aag gct gtg	1059
Thr Thr Glu Lys Lys Thr Glu Gln Gln Arg Arg Arg Glu Lys Ala Val	
335 340 345	

cac agg ctg cgg gta cag cag gcc gcg ttg cgg gcc gcc cgg ctc cgg 1107
 His Arg Leu Arg Val Gln Gln Ala Ala Leu Arg Ala Ala Arg Leu Arg
 350 355 360
 cac cag gag ctg ttc cgg ctg cgc ggg atc aag gcc cag gtg gcc ctg 1155
 His Gln Glu Leu Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala Leu
 365 370 375 380
 agg ctg gcg gag ctg gcg cgg cgg cag agg cgg cgg cag gcg cgg cgg 1203
 Arg Leu Ala Glu Leu Ala Arg Arg Gln Arg Arg Arg Gln Ala Arg Arg
 385 390 395
 gag gct gag gct gac aag ccc cga agg ctg ggg cgg ctc aag tac cag 1251
 Glu Ala Glu Ala Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln
 400 405 410
 gca cct gac atc gac gtg cag ctg agc tcg gag ctg aca gac tcg ctc 1299
 Ala Pro Asp Ile Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu
 415 420 425
 agg acc ctg aag ccc gag ggc aac atc ctt cga gac cgg ttc aag agc 1347
 Arg Thr Leu Lys Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser
 430 435 440
 ttc cag agg agg aat atg atc gag cct cga gag aga gcc aag ttc aaa 1395
 Phe Gln Arg Arg Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys
 445 450 455 460
 cgc aag tac aag gtg aag ctg gtg gag aag cgg gcg ttc cgt gag atc 1443
 Arg Lys Tyr Lys Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile
 465 470 475
 cag ttg tagctgccat cagatgccgg agactgcccc ttcaataaaaa aatctcttct 1499
 Gln Leu
 agctcaaaaa aaaaaaaaaa a 1520

<210> 108

<211> 478

<212> PRT

<213> Homo sapiens

<400> 108

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 Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr Ser Val Asp Pro
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 Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys Lys Arg Gly Trp
 35 40 45
 Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val Asp Gln Phe Leu
 50 55 60
 Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly Leu Leu Ser Glu
 65 70 75 80
 Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly Ser Lys Glu Lys
 85 90 95
 Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys Ser Leu Leu Leu
 100 105 110
 Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn Thr Ser Lys Val
 115 120 125
 Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro Asn Ala Lys Lys
 130 135 140
 Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala Lys Gln Gly Glu
 145 150 155 160
 Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu Leu Asn Pro Ser
 165 170 175
 Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val Glu Arg Pro Phe
 180 185 190
 Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg Pro Leu Val Gly
 195 200 205
 Gln Asp Glu Phe Phe Leu Glu Gln Thr Lys Lys Lys Gly Val Lys Arg
 210 215 220
 Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro Ala Val Glu Val

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225          230          235          240
Ala Pro Ala Gly Ala Ser Tyr Asn Pro Ser Phe Glu Asp His Gln Thr
          245          250          255
Leu Leu Ser Ala Ala His Glu Val Glu Leu Gln Arg Gln Lys Glu Ala
          260          265          270
Glu Lys Leu Glu Arg Gln Leu Ala Leu Pro Ala Thr Glu Gln Ala Ala
          275          280          285
Thr Gln Glu Ser Thr Phe Gln Glu Leu Cys Glu Gly Leu Leu Glu Glu
          290          295          300
Ser Asp Gly Glu Gly Glu Pro Gly Gln Gly Glu Gly Pro Glu Ala Gly
305          310          315          320
Asp Ala Glu Val Cys Pro Thr Pro Ala Arg Leu Ala Thr Thr Glu Lys
          325          330          335
Lys Thr Glu Gln Gln Arg Arg Arg Glu Lys Ala Val His Arg Leu Arg
          340          345          350
Val Gln Gln Ala Ala Leu Arg Ala Ala Arg Leu Arg His Gln Glu Leu
          355          360          365
Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala Leu Arg Leu Ala Glu
370          375          380
Leu Ala Arg Arg Gln Arg Arg Arg Gln Ala Arg Arg Glu Ala Glu Ala
385          390          395          400
Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln Ala Pro Asp Ile
          405          410          415
Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu Arg Thr Leu Lys
          420          425          430
Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser Phe Gln Arg Arg
          435          440          445
Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys Arg Lys Tyr Lys
          450          455          460
Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile Gln Leu
465          470          475

<210> 109
<211> 1789
<212> DNA
<213> Homo sapiens

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<222> 95..1252

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<222> 1253..1789

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<222> 1751..1756

<220>
<221> polyA_site
<222> 1774..1789

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tctgccaagc ttctccgata cccaggtttc ataa atg tgt ttg ttg ctt tcc tgc 115
Met Cys Leu Leu Leu Ser Cys
-10
cct tgc cac ccc tct gcc cac gga cag tcc atg tgg att gag aga acc 163

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Pro	Cys	His	Pro	Ser	Ala	His	Gly	Gln	Ser	Met	Trp	Ile	Glu	Arg	Thr	
	-5						1				5					
tcc	ttc	gtg	act	gca	tac	aag	ctg	ccg	ggg	atc	ctg	cgc	tgg	ttt	gag	211
Ser	Phe	Val	Thr	Ala	Tyr	Lys	Leu	Pro	Gly	Ile	Leu	Arg	Trp	Phe	Glu	
10				15					20					25		
gtg	gtg	cac	atg	tcg	cag	acc	aca	att	agt	cct	ctg	gag	aat	gcc	ata	259
Val	Val	His	Met	Ser	Gln	Thr	Thr	Ile	Ser	Pro	Leu	Glu	Asn	Ala	Ile	
			30						35					40		
gaa	acc	atg	tcc	acg	gcc	aat	gag	aag	atc	ctg	atg	atg	ata	aac	cag	307
Glu	Thr	Met	Ser	Thr	Ala	Asn	Glu	Lys	Ile	Leu	Met	Met	Ile	Asn	Gln	
			45					50					55			
tac	cag	agt	gat	gag	acc	ctc	ccc	atc	aac	cca	ctc	tcc	atg	ctc	ctg	355
Tyr	Gln	Ser	Asp	Glu	Thr	Leu	Pro	Ile	Asn	Pro	Leu	Ser	Met	Leu	Leu	
	60						65					70				
aac	ggg	att	gtg	gac	cct	gct	gtc	atg	gga	ggc	ttc	gcc	aag	tat	gag	403
Asn	Gly	Ile	Val	Asp	Pro	Ala	Val	Met	Gly	Gly	Phe	Ala	Lys	Tyr	Glu	
75						80					85					
aag	gcc	ttc	ttc	act	gaa	gag	tat	gtc	agg	gac	cac	cct	gag	gac	cag	451
Lys	Ala	Phe	Phe	Thr	Glu	Glu	Tyr	Val	Arg	Asp	His	Pro	Glu	Asp	Gln	
90				95					100					105		
gac	aag	ctg	acc	cac	ctc	aag	gac	ctg	att	gca	tgg	cag	atc	ccc	ttc	499
Asp	Lys	Leu	Thr	His	Leu	Lys	Asp	Leu	Ile	Ala	Trp	Gln	Ile	Pro	Phe	
				110					115					120		
ttg	gga	gct	ggg	att	aag	atc	cat	gag	aaa	agg	gtg	tca	gat	aac	ttg	547
Leu	Gly	Ala	Gly	Ile	Lys	Ile	His	Glu	Lys	Arg	Val	Ser	Asp	Asn	Leu	
			125					130					135			
cga	ccc	ttc	cat	gac	cgg	atg	gag	gaa	tgt	ttc	aag	aac	ctg	aaa	atg	595
Arg	Pro	Phe	His	Asp	Arg	Met	Glu	Glu	Cys	Phe	Lys	Asn	Leu	Lys	Met	
	140					145					150					
aag	gtg	gag	aag	gag	tac	ggt	gtc	cga	gag	atg	cct	gac	ttt	gac	gac	643
Lys	Val	Glu	Lys	Glu	Tyr	Gly	Val	Arg	Glu	Met	Pro	Asp	Phe	Asp	Asp	
155					160						165					
agg	aga	gtg	ggc	cgt	ccc	agg	tct	atg	ctg	cgc	tca	tac	aga	cag	atg	691
Arg	Arg	Val	Gly	Arg	Pro	Arg	Ser	Met	Leu	Arg	Ser	Tyr	Arg	Gln	Met	
170				175					180					185		
tcc	atc	atc	tct	ctg	gct	tcc	atg	aat	tct	gac	tgc	agc	acc	ccc	agc	739
Ser	Ile	Ile	Ser	Leu	Ala	Ser	Met	Asn	Ser	Asp	Cys	Ser	Thr	Pro	Ser	
				190					195					200		
aag	cct	acc	tca	gag	agc	ttt	gac	ctg	gaa	tta	gca	tca	ccc	aag	acg	787
Lys	Pro	Thr	Ser	Glu	Ser	Phe	Asp	Leu	Glu	Leu	Ala	Ser	Pro	Lys	Thr	
		205						210				215				
ccg	aga	gtg	gag	cag	gag	gaa	ccg	atc	tcc	ccg	ggg	agc	acc	ctg	cct	835
Pro	Arg	Val	Glu	Gln	Glu	Glu	Pro	Ile	Ser	Pro	Gly	Ser	Thr	Leu	Pro	
	220					225						230				
gag	gtc	aag	ctg	cgg	agg	tcc	aag	aag	agg	aca	aag	aga	agc	agc	gta	883
Glu	Val	Lys	Leu	Arg	Arg	Ser	Lys	Lys	Arg	Thr	Lys	Arg	Ser	Ser	Val	
	235			240							245					
gtt	ttt	gcg	gat	gag	aaa	gca	gct	gca	gag	tcg	gac	ctg	aag	cgg	ctt	931
Val	Phe	Ala	Asp	Glu	Lys	Ala	Ala	Ala	Glu	Ser	Asp	Leu	Lys	Arg	Leu	
250				255					260					265		
tcc	agg	aag	cat	gag	ttc	atg	agt	gac	acc	aac	ctc	tcg	gag	cat	gcg	979
Ser	Arg	Lys	His	Glu	Phe	Met	Ser	Asp	Thr	Asn	Leu	Ser	Glu	His	Ala	
				270				275						280		
gcc	atc	ccc	ctc	aag	gcg	tct	gtc	ctc	tct	caa	atg	agc	ttt	gcc	agc	1027
Ala	Ile	Pro	Leu	Lys	Ala	Ser	Val	Leu	Ser	Gln	Met	Ser	Phe	Ala	Ser	
		285					290					295				
cag	tcc	atg	cct	acc	atc	cca	gcc	ctg	gcg	ctc	tca	gtg	gca	ggc	atc	1075
Gln	Ser	Met	Pro	Thr	Ile	Pro	Ala	Leu	Ala	Leu	Ser	Val	Ala	Gly	Ile	
	300					305					310					
cct	ggg	ttg	gat	gag	gcc	aac	aca	tct	ccc	cgc	ctc	agc	cag	acc	ttc	1123
Pro	Gly	Leu	Asp	Glu	Ala	Asn	Thr	Ser	Pro	Arg	Leu	Ser	Gln	Thr	Phe	
	315				320					325						
ctc	caa	ctc	tca	gat	ggt	gac	aag	aag	aca	ctc	aca	cgg	aag	aag	gtc	1171

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 Asn Gln Phe Phe Lys Thr Met Leu Ala Ser Lys Ser Ala Glu Glu Gly
 350 355 360
 aaa cag atc cca gac tcg ctg tcc acg gac ctg tgagctgctg ctgactaggg 1272
 Lys Gln Ile Pro Asp Ser Leu Ser Thr Asp Leu
 365 370
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 aagcctcaga gagtgggaga ctgtcccat cagttgtcct tacttagagg agacagagag 1392
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 ctcccagtgt gctctcccca acatcctagg cacagctttc ataaccagc ttcttaggtg 1572
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 <212> PRT
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 Gly Ile Leu Arg Trp Phe Glu Val Val His Met Ser Gln Thr Thr Ile
 20 25 30
 Ser Pro Leu Glu Asn Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys
 35 40 45
 Ile Leu Met Met Ile Asn Gln Tyr Gln Ser Asp Glu Thr Leu Pro Ile
 50 55 60 65
 Asn Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met
 70 75 80
 Gly Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val
 85 90 95
 Arg Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu
 100 105 110
 Ile Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys Ile His Glu
 115 120 125
 Lys Arg Val Ser Asp Asn Leu Arg Pro Phe His Asp Arg Met Glu Glu
 130 135 140 145
 Cys Phe Lys Asn Leu Lys Met Lys Val Glu Lys Glu Tyr Gly Val Arg
 150 155 160
 Glu Met Pro Asp Phe Asp Asp Arg Arg Val Gly Arg Pro Arg Ser Met
 165 170 175
 Leu Arg Ser Tyr Arg Gln Met Ser Ile Ile Ser Leu Ala Ser Met Asn
 180 185 190
 Ser Asp Cys Ser Thr Pro Ser Lys Pro Thr Ser Glu Ser Phe Asp Leu
 195 200 205
 Glu Leu Ala Ser Pro Lys Thr Pro Arg Val Glu Gln Glu Glu Pro Ile
 210 215 220 225
 Ser Pro Gly Ser Thr Leu Pro Glu Val Lys Leu Arg Arg Ser Lys Lys
 230 235 240
 Arg Thr Lys Arg Ser Ser Val Val Phe Ala Asp Glu Lys Ala Ala Ala
 245 250 255
 Glu Ser Asp Leu Lys Arg Leu Ser Arg Lys His Glu Phe Met Ser Asp

260 265 270
 Thr Asn Leu Ser Glu His Ala Ala Ile Pro Leu Lys Ala Ser Val Leu
 275 280 285
 Ser Gln Met Ser Phe Ala Ser Gln Ser Met Pro Thr Ile Pro Ala Leu
 290 295 300 305
 Ala Leu Ser Val Ala Gly Ile Pro Gly Leu Asp Glu Ala Asn Thr Ser
 310 315 320
 Pro Arg Leu Ser Gln Thr Phe Leu Gln Leu Ser Asp Gly Asp Lys Lys
 325 330 335
 Thr Leu Thr Arg Lys Lys Val Asn Gln Phe Phe Lys Thr Met Leu Ala
 340 345 350
 Ser Lys Ser Ala Glu Glu Gly Lys Gln Ile Pro Asp Ser Leu Ser Thr
 355 360 365
 Asp Leu
 370

<210> 111
 <211> 1408
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..102

<220>
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 <222> 103..1263

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 <221> 3'UTR
 <222> 1264..1408

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 <222> 1341..1346

<220>
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 <222> 1365..1408

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 Met Ser Thr Phe
 1
 ttc tcg gac aca gca tgg atc tgc ctg gct gtc ccc aca gta cta tgt 162
 Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro Thr Val Leu Cys
 5 10 15 20
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 Gly Thr Val Phe Cys Lys Tyr Lys Lys Ser Ser Gly Gln Leu Trp Ser
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 Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys Leu Leu Ile Leu
 40 45 50
 tcc cct ttt tgg ggc ttg atc ctc ttc tcg gtg tca tgc ttc ctc atg 306
 Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser Cys Phe Leu Met
 55 60 65
 tat act tac tta tct ggc caa gaa ttg tta cct gtg gat cag aag gca 354
 Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val Asp Gln Lys Ala
 70 75 80
 gtc ctg gtg aca ggt ggt gat tgc ggg ctt ggc cat gct ttg tgc aag 402
 Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His Ala Leu Cys Lys

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Tyr Leu Asp Glu Gly Phe Thr Val Phe Ala Gly Val Leu Asn Glu							
	105		110		115		
aat ggc cca gga gct gag gaa ttg cga aga acc tgc tct ccg cgc ctc							498
Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys Ser Pro Arg Leu							
	120		125		130		
tcg gtg ctc caa atg gac atc acg aag cca gtg cag ata aaa gat gct							546
Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln Ile Lys Asp Ala							
	135		140		145		
tac agc aag gtt gca gca atg ctg cag gac aga gga ctg tgg gct gtg							594
Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly Leu Trp Ala Val							
	150		155		160		
atc aac aat gct ggg gtg ctt ggc ttt cca act gat ggg gag ctt ctt							642
Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp Gly Glu Leu Leu							
	165		170		175		180
ctt atg act gac tac aaa caa tgc atg gcc gtg aac ttc ttt gga act							690
Leu Met Thr Asp Tyr Lys Gln Cys Met Ala Val Asn Phe Phe Gly Thr							
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gtg gag gtc aca aag acg ttt ttg cct ctt ctt aga aaa tcc aaa ggg							738
Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg Lys Ser Lys Gly							
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agg ctg gtg aat gtc agc agc atg gga gga ggg gcc cca gtg gaa agg							786
Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala Pro Val Glu Arg							
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ctg gca tct tat ggc tca tca aag gcg gct gtg acc atg ttc tca tca							834
Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr Met Phe Ser Ser							
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gtt atg aga ctg gag ctt tcc aag tgg gga att aaa gtt gct tcc atc							882
Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys Val Ala Ser Ile							
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caa cct gga ggc ttc cta aca aat atc gca ggc acc agt gac aag tgg							930
Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr Ser Asp Lys Trp							
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gaa aag ctg gag aag gac att ctg gac cac ctc ccc gct gag gta cag							978
Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro Ala Glu Val Gln							
	280		285		290		
gaa gac tac tgc cag gac tac atc tta gca cag cgg aat ttc ctc cta							1026
Glu Asp Tyr Cys Gln Asp Tyr Ile Leu Ala Gln Arg Asn Phe Leu Leu							
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Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro Val Leu Arg Asp							
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atc cag cat gct atc ttg gcg aag agc cct ttt gcc tat tac acg cca							1122
Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala Tyr Tyr Thr Pro							
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ggg aaa ggc gct tac ttg tgg atc tgc ctt gct cac tat ttg cct att							1170
Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His Tyr Leu Pro Ile							
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ggc ata tat gat tac ttt gct aaa aga cat ttt ggc caa gac aag ccc							1218
Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly Gln Asp Lys Pro							
	360		365		370		
atg ccc aga gct tta aga atg cct aac tac aag aaa aag gcc ccc							1263
Met Pro Arg Ala Leu Arg Met Pro Asn Tyr Lys Lys Lys Ala Pro							
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35 40 45
Leu Leu Ile Leu Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser
50 55 60
Cys Phe Leu Met Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val
65 70 75 80
Asp Gln Lys Ala Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His
85 90 95
Ala Leu Cys Lys Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly
100 105 110
Val Leu Asn Glu Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys
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Ser Pro Arg Leu Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln
130 135 140
Ile Lys Asp Ala Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly
145 150 155 160
Leu Trp Ala Val Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp
165 170 175
Gly Glu Leu Leu Leu Met Thr Asp Tyr Lys Gln Cys Met Ala Val Asn
180 185 190
Phe Phe Gly Thr Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg
195 200 205
Lys Ser Lys Gly Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala
210 215 220
Pro Val Glu Arg Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr
225 230 235 240
Met Phe Ser Ser Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys
245 250 255
Val Ala Ser Ile Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr
260 265 270
Ser Asp Lys Trp Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro
275 280 285
Ala Glu Val Gln Glu Asp Tyr Cys Gln Asp Tyr Ile Leu Ala Gln Arg
290 295 300
Asn Phe Leu Leu Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro
305 310 315 320
Val Leu Arg Asp Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala
325 330 335
Tyr Tyr Thr Pro Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His
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Tyr Leu Pro Ile Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly
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 Met Gly Arg Thr
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 Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp Glu Asn Glu Lys
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 Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser
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